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METHODS FOR EVALUATING OLIGONUCLEOTIDE PROBE SEQUENCES

Appendix

This patent application includes an appendix (the "Appendix"), which contains the source code for the software used in carrying out the examples in accordance with the present invention.

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BACKGROUND OF THE INVENTION

1. Field of the Invention.

Significant morbidity and mortality are associated with infectious diseases and genetically inherited disorders. More rapid and accurate diagnostic methods are required for better monitoring and treatment of these conditions. Molecular methods using DNA probes, nucleic acid hybridization and *in vitro* amplification techniques are promising methods offering advantages to conventional methods used for patient diagnoses.

Nucleic acid hybridization has been employed for investigating the identity and establishing the presence of nucleic acids. Hybridization is based on

complementary base pairing. When complementary single stranded nucleic acids are incubated together, the complementary base sequences pair to form double-stranded hybrid molecules. The ability of single stranded deoxyribonucleic acid (ssDNA) or ribonucleic acid (RNA) to form a hydrogen bonded structure with a complementary nucleic acid sequence has been employed as an analytical tool in molecular biology research. The availability of radioactive nucleoside triphosphates of high specific activity and the development of methods for their incorporation into DNA and RNA has made it possible to identify, isolate, and characterize various nucleic acid sequences of biological interest. Nucleic acid hybridization has great potential in diagnosing disease states associated with unique nucleic acid sequences. These unique nucleic acid sequences may result from genetic or environmental change in DNA by insertions, deletions, point mutations, or by acquiring foreign DNA or RNA by means of infection by bacteria, molds, fungi, and viruses. The application of nucleic acid hybridization as a diagnostic tool in clinical medicine is limited due to the cost and effort associated with the development of sufficiently sensitive and specific methods for detecting potentially low concentrations of disease-related DNA or RNA present in the complex mixture of nucleic acid sequences found in patient samples.

One method for detecting specific nucleic acid sequences generally involves immobilization of the target nucleic acid on a solid support such as nitrocellulose paper, cellulose paper, diazotized paper, or a nylon membrane. After the target nucleic acid is fixed on the support, the support is contacted with a suitably labeled probe nucleic acid for about two to forty-eight hours. After the above time period, the solid support is washed several times at a controlled temperature to remove unhybridized probe. The support is then dried and the hybridized material is detected by autoradiography or by spectrometric methods. When very low concentrations must be detected, the above method is slow and labor intensive, and nonisotopic labels that are less readily detected than radiolabels are frequently not suitable.

A method for the enzymatic amplification of specific segments of DNA known as the polymerase chain reaction (PCR) method has been described. This *in vitro* amplification procedure is based on repeated cycles of denaturation, oligonucleotide primer annealing, and primer extension by thermophilic

polymerase, resulting in the exponential increase in copies of the region flanked by the primers. The PCR primers, which anneal to opposite strands of the DNA, are positioned so that the polymerase catalyzed extension product of one primer can serve as a template strand for the other, leading to the accumulation of a  
5 discrete fragment whose length is defined by the distance between the 5' ends of the oligonucleotide primers.

Other methods for amplifying nucleic acids have also been developed. These methods include single primer amplification, ligase chain reaction (LCR), transcription-mediated amplification methods including 3SR and NASBA, and the  
10 Q-beta-replicase method. Regardless of the amplification used, the amplified product must be detected.

One method for detecting nucleic acids is to employ nucleic acid probes that have sequences complementary to sequences in the target nucleic acid. A nucleic acid probe may be, or may be capable of being, labeled with a reporter group or may be, or may be capable of becoming, bound to a support. Detection of signal depends upon the nature of the label or reporter group. Usually, the probe is comprised of natural nucleotides such as ribonucleotides and deoxyribonucleotides and their derivatives although unnatural nucleotide mimetics such as peptide nucleic acids and oligomeric nucleoside phosphonates are also  
15 used. Commonly, binding of the probes to the target is detected by means of a label incorporated into the probe. Alternatively, the probe may be unlabeled and the target nucleic acid labeled. Binding can be detected by separating the bound probe or target from the free probe or target and detecting the label. In one approach, a sandwich is formed comprised of one probe, which may be labeled, the target and a probe that is or can become bound to a surface. Alternatively,  
20 binding can be detected by a change in the signal-producing properties of the label upon binding, such as a change in the emission efficiency of a fluorescent or chemiluminescent label. This permits detection to be carried out without a separation step. Finally, binding can be detected by labeling the target, allowing  
25 the target to hybridize to a surface-bound probe, washing away the unbound target and detecting the labeled target that remains.  
30

Direct detection of labeled target hybridized to surface-bound probes is particularly advantageous if the surface contains a mosaic of different probes that

are individually localized to discrete, known areas of the surface. Such ordered arrays containing a large number of oligonucleotide probes have been developed as tools for high throughput analyses of genotype and gene expression.

Oligonucleotides synthesized on a solid support recognize uniquely

complementary nucleic acids by hybridization, and arrays can be designed to define specific target sequences, analyze gene expression patterns or identify specific allelic variations. One difficulty in the design of oligonucleotide arrays is that oligonucleotides targeted to different regions of the same gene can show large differences in hybridization efficiency, presumably due, at least in part, to the interplay between the secondary structures of the oligonucleotides and their targets and the stability of the final probe/target hybridization product. A method for predicting which oligonucleotides will show detectable hybridization would substantially decrease the number of iterations required for optimal array design and would be particularly useful when the total number of oligonucleotide probes on the array is limited. A method to predict oligonucleotide hybridization efficiency would also streamline the empirical approaches currently used to select potential antisense therapeutics, which are designed to modulate gene expression *in vivo* by hybridizing to specific messenger RNA (mRNA) molecules and inhibiting their translation into proteins.

While it is well known that the structure of the target nucleic acid affects the affinity of oligonucleotide hybridization, current methods for predicting target structures from the primary sequence fail to predict target regions accessible for oligonucleotide binding. Consequently, selection of oligonucleotides for antisense reagents or oligonucleotide probe arrays has been largely empirical. As most of the target sequence is sequestered by intramolecular base pairing and not accessible for oligonucleotide binding, the process of identifying good oligonucleotides has required large numbers of low efficiency experiments.

The design and implementation of algorithms that effectively predict the ability of oligonucleotides to rapidly and avidly bind to complementary nucleotide sequences has been an important problem in molecular biology since the invention of facile methods for chemical DNA synthesis. The subsequent inventions of the polymerase chain reaction (PCR), antisense inhibition of gene expression and oligonucleotide array methods for performing massively parallel

hybridization experiments have made the need for effective predictive algorithms even more critical.

Previous attempts to solve the nucleic acid probe design problem include PCR primer design software applications (e.g., OLIGO®), neural networks, PCR primer design applications that search for sequences that possess minimal ability to cross-hybridize with other targets present in a sample (e.g., HYBsimulator™), and approaches that attempt to predict the efficiency of antisense sequence suppression of mRNA translation from a combination of predicted nucleic acid duplex melting temperature and predicted target strand structure. The methods that predict effective oligonucleotide primers for performing PCR from DNA templates work well for that application where relatively stringent conditions are employed. This is because PCR experimental design greatly simplifies the prediction problem: hybridization is performed at high temperature, at relatively low ionic strength and in the presence of a large molar excess of oligonucleotide. Under these conditions, the oligonucleotide and target secondary structures are relatively unimportant.

Unfortunately, these conditions do not apply to oligonucleotide arrays, which are usually hybridized under relatively non-denaturing conditions, or to antisense suppression of gene expression, which takes place *in vivo*. Oligonucleotide arrays can contain hundreds of thousands of different sequences and conditions are chosen to allow the oligonucleotide with the lowest melting temperature to hybridize efficiently. These "lowest common denominator" conditions are usually relatively non-denaturing and secondary structure constraints become significant. Accordingly, the above applications require new predictive methods that are capable of estimating the effects of oligonucleotide and target structure on hybridization efficiency. For these reasons, current algorithms for designing PCR primer oligonucleotides fail badly when applied to the problems of oligonucleotide array or antisense oligonucleotide design.

To date, the most effective approach for identifying oligonucleotides with good hybridization efficiency has been an empirical one. Such an approach involves the synthesis of large numbers of oligonucleotide probes for a given target nucleotide sequence. Arrays are formed that include the above oligonucleotide probes. Hybridization experiments are carried out to determine

which of the oligonucleotide probes exhibit good hybridization efficiencies. Examples of such an approach are found in D. Lockhart, et al., Nature Biotech., *infra*, L. Wodicka, et al., Nature Biotechnology, *infra.*, and N. Milner et al. Nature Biotech., *infra*. One major drawback to this approach is the vast number of  
5 oligonucleotides that must be synthesized in order to achieve a satisfactory result. Typically, about 2%-5% of the test probes synthesized yield acceptable signal levels.

The use of neural networks for oligonucleotide design has also been investigated. Neural networks are easily taught with real data; they therefore  
10 afford a general approach to many problems. However, their performance is limited by the "senses" that they are given. An analogy works best here: the human brain is an astoundingly capable neural network, but a blind person cannot be taught to reliably distinguish colors by smell. In addition, a large amount of data is required to adequately teach a neural network to perform its job well. A  
15 comprehensive database for either oligonucleotide array design or antisense suppression of gene expression has not been made available. For these reasons, the performance reported to-date of neural network solutions against the probe design problem is mediocre.

Finally, approaches that have attempted to use target nucleic acid folding  
20 calculations to predict experimental results inferred to depend upon hybridization efficiency (e.g. antisense suppression of mRNA translation) have so far only demonstrated that the predictions of current nucleic acid folding calculations correlate poorly with observed behavior. The probable reason for this is that the structures predicted by such programs for long sequences are poor predictors of  
25 chemical reality; the results of experiments that attempt to confirm the predictions of such calculations support this assessment. Recent improvements to this approach which use predicted RNA structure topology as a predictor of relative RNA/RNA association kinetics have been more successful at forecasting the results of antisense experiments. However, these methods are not  
30 computationally efficient, and have so far only been shown to work for targets less than 100 bases long. Such methods are therefore not yet capable of predicting the behavior of full-length mRNA targets, which are typically between 1,000 and 2,000 bases in length.

2. Description of the Related Art.

U.S. Patent No. 5,512,438 (Ecker) discloses the inhibition of RNA expression by forming a pseudo-half knot RNA at the target's RNA secondary structure using antisense oligonucleotides.

Cook, *et al.*, in U.S. Patent No. 5,670,633 discuss sugar-modified oligonucleotides that detect and modulate gene expression.

Antisense oligonucleotide inhibition of the RAS gene is disclosed in U.S. Patent No. 5,582,986 (Monia, *et al.*).

U.S. Patent No. 5,593,834 (Lane, *et al.*) discusses a method of preparing DNA sequences with known ligand binding characteristics.

Mitsuhashi, *et al.*, in U.S. Patent No. 5,556,749 discusses a computerized method for designing optimal DNA probes and an oligonucleotide probe design station.

U.S. Patent No. 5,081,584 (Omichinski, *et al.*) discloses a computer-assisted design of anti-peptides based on the amino acid sequence of a target peptide.

A PCR primer design application that searches for sequences that possess minimal ability to cross-hybridize with other targets present in a sample is available as HYBsimulator™, version 2.0, AGCT, Inc., 2102 Business Center Drive, Suite 170, Irvine, CA 92715 (714) 833-9983.

A PCR primer design software application is available as OLIGO®, version 5.0, National Biosciences, Inc., 3650 Annapolis Lane North, #140, Plymouth, MN 55447 (800) 747-4362.

D. J. Lockhart, *et al.*, Nature Biotech. 14:1675-1684 (1996) describe a neural network approach to the selection of efficient surface-bound oligonucleotide probes.

M. Mitsuhashi, *et al.*, Nature, 367:759-761 (1994) disclose a method for designing specific oligonucleotide probes and primers by modeling the potential cross-hybridization of candidate probes to non-target sequences known to be present in samples.

R. A. Stull, *et al.*, Nuc. Acids Res., 20:3501-3508 (1992) describe a method of predicting the efficacy of antisense oligonucleotides, using predicted target

secondary structure and predicted oligonucleotide/target binding free energy as input parameters.

N. Milner, *et al.*, Nature Biotechnology, 15:537-541 (1997) compare observed patterns of probe hybridization to those expected from the predicted secondary structure of the nucleic acid target.

L. Wodicka, *et al.*, Nature Biotechnology, 15:1359-1367 (1997) describe simple rules for avoiding inefficient and non-specific probes during design and synthesis of oligonucleotides arrays.

J. SantaLucia Jr., *et al.*, Biochemistry, 35:3555 (1996) disclose parameters and methods for the calculation of thermodynamic properties of DNA/DNA homoduplexes.

N. Sugimoto, *et al.*, Biochemistry, 34:11211 (1995) disclose parameters and methods for the calculation of thermodynamic properties of DNA/RNA heteroduplexes.

J.A. Jaeger, *et al.*, Proc. Natl. Acad. Sci. USA, 86:7706 (1989) disclose methods for estimation of the free energy of the most stable intramolecular structure of a single-stranded polynucleotide, by means of a dynamic programming algorithm.

S. F. Altschul, *et al.*, Nature Genetics, 6:119-129 (1994) disclose methods for calculating the complexity and information content of amino acid and nucleic acid sequences.

T. A. Weber and E. Helfand, J. Chem. Phys., 71, 4760 (1979) describe approaches for the modeling of polymer structures by molecular dynamics simulations.

V. Patzel and G. Sczakiel, Nature Biotech., 16, 64-68 (1998) disclose methods for estimating rate constants for association of antisense RNA molecules with mRNA targets by examination of predicted antisense RNA secondary structures.

Light-generated oligonucleotide arrays for rapid DNA sequence analysis is described by A. C. Pease, *et al.*, Proc. Nat. Acad. Sci. USA (1994) 91:5022-5026.

Mitsuhashi discusses basic requirements for designing optimal oligonucleotide probe sequences in J. Clinical Laboratory Analysis (1996) 10:277-284.

Rychlik, *et al.*, discloses a computer program for choosing optimal oligonucleotides for filter hybridization, sequencing and in vitro amplification of DNA in Nucleic Acids Research (1989) 17(21):8543-8551.

5 A strategy for designing specific antisense oligonucleotide sequences is described by Mitsuhashi in J. Gastroenterol. (1997) 32:282-287.

Mitsuhashi discusses basic requirements for designing optimal PCR primers in J. Clinical Laboratory Analysis (1996) 10:285-293.

10 Hyndman, *et al.*, disclose software to determine optimal oligonucleotide sequences based on hybridization simulation data in BioTechniques (1996) 20(6):1090-1094.

Eberhardt discloses a shell program for the design of PCR primers using genetics computer group (GCG) software (7.1) on VAX/VMS™ systems in BioTechniques (1992) 13(6):914-917.

15 Chen, *et al.*, disclose a computer program for calculating the melting temperature of degenerate oligonucleotides used in PCR or hybridization in BioTechniques (1997) 22(6):1158-1160.

20 Partial thermodynamic parameters for prediction stability and washing behavior of DNA duplexes immobilized on gel matrix is described by Kunitsyn, *et al.*, in J. Biomolecular Structure & Dynamics, ISSN 0739-1102 (1996) 14(1):239-244.

#### SUMMARY OF THE INVENTION

One embodiment of the present invention is a method for predicting the potential of an oligonucleotide to hybridize to a target nucleotide sequence. A  
25 predetermined set of unique oligonucleotide sequences is identified. The unique oligonucleotide sequences are chosen to sample the entire length of a nucleotide sequence that is hybridizable with the target nucleotide sequence. At least one parameter that is predictive of the ability of each of the oligonucleotides specified by the set of sequences to hybridize to the target nucleotide sequence is  
30 determined and evaluated for each of the above oligonucleotide sequences. A subset of oligonucleotide sequences within the predetermined set of unique oligonucleotide sequences is identified based on the examination of the parameter values. Finally, oligonucleotide sequences in the subset are identified that are

clustered along one or more regions of the nucleotide sequence that is hybridizable to the target nucleotide sequence. The oligonucleotide probes corresponding to the identified sequences find use in polynucleotide assays particularly where the assays involve oligonucleotide arrays. For a discussion of  
5 oligonucleotide arrays, see, e.g., U.S. Patent No. 5,700,637 (E. Southern) and U.S. Patent No. 5,667,667 (E. Southern), the relevant disclosures of which are incorporated herein by reference.

Another embodiment of the present invention is a method for predicting the potential of an oligonucleotide to hybridize to a complementary target nucleotide  
10 sequence. A set of overlapping oligonucleotide sequences is identified based on a nucleotide sequence that is complementary to the target nucleotide sequence. At least two parameters that are independently predictive of the ability of each of the oligonucleotides specified by the oligonucleotide sequences to hybridize to the target nucleotide sequence are determined and evaluated for each of the  
15 oligonucleotide sequences. Independence is assured by requiring that the parameters be poorly correlated with respect to one another. A subset of oligonucleotide sequences within the set of oligonucleotide sequences is identified based on the examination of the parameter values. Finally, oligonucleotide sequences in the subset are identified that are clustered along one or more  
20 regions of the nucleotide sequence that is complementary to the target nucleotide sequence.

Another embodiment of the present invention is a method for predicting the potential of an oligonucleotide to hybridize to a complementary target nucleotide sequence. A set of overlapping oligonucleotide sequences is obtained based on a  
25 nucleotide sequence of length L, complementary to the target nucleotide sequence. The oligonucleotide sequences of the set of overlapping oligonucleotide sequences are of identical length N and spaced one nucleotide apart. The set comprises L-N+1 oligonucleotide sequences. Parameters are determined for each of the oligonucleotide sequences of the set of overlapping  
30 oligonucleotide sequences. One parameter is the predicted melting temperature of the duplex of each of the oligonucleotides specified by the oligonucleotide sequences and the target nucleotide sequence, corrected for salt concentration. The other parameter is the predicted free energy of the most stable intramolecular

structure of each of the oligonucleotides specified by the oligonucleotide sequences at the temperature of hybridization of the oligonucleotide with the target nucleotide sequence. A subset of oligonucleotide sequences within the set of oligonucleotide sequences is selected based on an examination of the  
5 parameter values by establishing cut-off values for each of the parameters. Oligonucleotide sequences in the subset that are clustered along one or more regions of the complementary nucleotide sequence are ranked based on the sizes of the clusters of oligonucleotide sequences. Finally, a subset of the clustered oligonucleotide sequences is selected that statistically samples the clusters of  
10 oligonucleotide sequences. The selected sampled subset is used to specify the synthesis of oligonucleotides for experimental evaluation.

Another aspect of the present invention is a computer based method for predicting the potential of an oligonucleotide to hybridize to a target nucleotide sequence. A predetermined number of unique oligonucleotides within a  
15 nucleotide sequence that is hybridizable with the target nucleotide sequence is identified under computer control. The oligonucleotides are chosen to sample the entire length of the nucleotide sequence. A value is determined and evaluated under computer control for each of the oligonucleotides for at least one parameter that is independently predictive of the ability of each of the oligonucleotides to  
20 hybridize to the target nucleotide sequence. The parameter values are stored. A subset of oligonucleotides within the predetermined number of unique oligonucleotides is identified by examination of the stored parameter values under computer control. Then, oligonucleotides in the subset that are clustered along a region of the nucleotide sequence that is hybridizable to the target nucleotide  
25 sequence are identified under computer control.

Another aspect of the present invention is a computer system for conducting a method for predicting the potential of an oligonucleotide to hybridize to a target nucleotide sequence. The system comprises (a) input means for introducing a target nucleotide sequence into the computer system, (b) means for  
30 determining a number of unique oligonucleotide sequences that are within a nucleotide sequence that is hybridizable with the target nucleotide sequence where the oligonucleotide sequences are chosen to sample the entire length of the nucleotide sequence, (c) memory means for storing the oligonucleotide

sequences, (d) means for controlling the computer system to carry out for each of the oligonucleotide sequences a determination and evaluation of a value for at least one parameter that is independently predictive of the ability of each of the oligonucleotide sequences to hybridize to the target nucleotide sequence, (e) means for storing the parameter values, (f) means for controlling the computer to carry out an identification from the stored parameter values a subset of oligonucleotide sequences within the number of unique oligonucleotide sequences based on the examination of the parameter, (g) means for storing the subset of oligonucleotides, (h) means for controlling the computer to carry out an identification of oligonucleotide sequences in the subset that are clustered along a region of the nucleotide sequence that is hybridizable to the target nucleotide sequence, (i) means for storing the oligonucleotide sequences in the subset, and (j) means for outputting data relating to the oligonucleotide sequences in the subset.

#### BRIEF DESCRIPTION OF THE DRAWINGS

Fig. 1 is a general flow chart depicting the method of the present invention.

Fig. 2 is a flow chart depicting a preferred embodiment of a method in accordance with the present invention.

Fig. 3 is a contour plot of normalized hybridization intensity from multiple experiments, as a function of the free energy of the most stable probe intramolecular structure ( $\Delta G_{MFOLD}$ ) and the difference between the predicted RNA/DNA heteroduplex melting temperature ( $T_m$ ) and the temperature of hybridization ( $T_{hyb}$ ).

Fig. 4 shows the observed hybridization patterns for oligonucleotides selected using a method in accordance with the present invention and additional oligonucleotides to a portion of the rabbit  $\beta$ -globin gene (radiolabeled antisense RNA target).

Fig. 5 shows the observed hybridization patterns for oligonucleotides selected using a method in accordance with the present invention and additional oligonucleotides to the HIV PRT gene (fluorescein-labeled sense RNA target).

Fig. 6 shows the observed hybridization patterns for oligonucleotides selected using a method in accordance with the present invention and additional oligonucleotides to the G3PDH gene (fluorescein-labeled antisense RNA target).

5 Fig. 7 shows the observed hybridization patterns for oligonucleotides selected using a method in accordance with the present invention and additional oligonucleotides to the p53 gene (fluorescein-labeled antisense RNA target).

Fig. 8 shows the observed hybridization patterns for oligonucleotides selected using a method in accordance with the present invention and additional oligonucleotides to the HIV PRTs gene (using data from the GeneChip™ data).

### 10 DEFINITIONS

Before proceeding further with a description of the specific embodiments of the present invention, a number of terms will be defined.

#### 15 Nucleic Acids:

Polynucleotide -- a compound or composition that is a polymeric nucleotide or nucleic acid polymer. The polynucleotide may be a natural compound or a synthetic compound. In the context of an assay, the polynucleotide is often referred to as a polynucleotide analyte. The polynucleotide can have from about  
20 20 to 5,000,000 or more nucleotides. The larger polynucleotides are generally found in the natural state. In an isolated state the polynucleotide can have about 30 to 50,000 or more nucleotides, usually about 100 to 20,000 nucleotides, more frequently 500 to 10,000 nucleotides. It is thus obvious that isolation of a polynucleotide from the natural state often results in fragmentation. The  
25 polynucleotides include nucleic acids, and fragments thereof, from any source in purified or unpurified form including DNA (dsDNA and ssDNA) and RNA, including tRNA, mRNA, rRNA, mitochondrial DNA and RNA, chloroplast DNA and RNA, DNA/RNA hybrids, or mixtures thereof, genes, chromosomes, plasmids, the genomes of biological material such as microorganisms, e.g., bacteria, yeasts,  
30 viruses, viroids, molds, fungi, plants, animals, humans, and the like. The polynucleotide can be only a minor fraction of a complex mixture such as a biological sample. Also included are genes, such as hemoglobin gene for sickle-cell anemia, cystic fibrosis gene, oncogenes, cDNA, and the like.

The polynucleotide can be obtained from various biological materials by procedures well known in the art. The polynucleotide, where appropriate, may be cleaved to obtain a fragment that contains a target nucleotide sequence, for example, by shearing or by treatment with a restriction endonuclease or other site specific chemical cleavage method.

For purposes of this invention, the polynucleotide, or a cleaved fragment obtained from the polynucleotide, will usually be at least partially denatured or single stranded or treated to render it denatured or single stranded. Such treatments are well known in the art and include, for instance, heat or alkali treatment, or enzymatic digestion of one strand. For example, dsDNA can be heated at 90-100° C. for a period of about 1 to 10 minutes to produce denatured material.

Target nucleotide sequence -- a sequence of nucleotides to be identified, usually existing within a portion or all of a polynucleotide, usually a polynucleotide analyte. The identity of the target nucleotide sequence generally is known to an extent sufficient to allow preparation of various sequences hybridizable with the target nucleotide sequence and of oligonucleotides, such as probes and primers, and other molecules necessary for conducting methods in accordance with the present invention, an amplification of the target polynucleotide, and so forth.

The target sequence usually contains from about 30 to 5,000 or more nucleotides, preferably 50 to 1,000 nucleotides. The target nucleotide sequence is generally a fraction of a larger molecule or it may be substantially the entire molecule such as a polynucleotide as described above. The minimum number of nucleotides in the target nucleotide sequence is selected to assure that the presence of a target polynucleotide in a sample is a specific indicator of the presence of polynucleotide in a sample. The maximum number of nucleotides in the target nucleotide sequence is normally governed by several factors: the length of the polynucleotide from which it is derived, the tendency of such polynucleotide to be broken by shearing or other processes during isolation, the efficiency of any procedures required to prepare the sample for analysis (e.g. transcription of a DNA template into RNA) and the efficiency of detection and/or amplification of the target nucleotide sequence, where appropriate.

Oligonucleotide -- a polynucleotide, usually single stranded, usually a synthetic polynucleotide but may be a naturally occurring polynucleotide. The oligonucleotide(s) are usually comprised of a sequence of at least 5 nucleotides, preferably, 10 to 100 nucleotides, more preferably, 20 to 50 nucleotides, and usually 10 to 30 nucleotides, more preferably, 20 to 30 nucleotides, and desirably about 25 nucleotides in length.

Various techniques can be employed for preparing an oligonucleotide. Such oligonucleotides can be obtained by biological synthesis or by chemical synthesis. For short sequences (up to about 100 nucleotides), chemical synthesis will frequently be more economical as compared to the biological synthesis. In addition to economy, chemical synthesis provides a convenient way of incorporating low molecular weight compounds and/or modified bases during specific synthesis steps. Furthermore, chemical synthesis is very flexible in the choice of length and region of the target polynucleotide binding sequence. The oligonucleotide can be synthesized by standard methods such as those used in commercial automated nucleic acid synthesizers. Chemical synthesis of DNA on a suitably modified glass or resin can result in DNA covalently attached to the surface. This may offer advantages in washing and sample handling. For longer sequences standard replication methods employed in molecular biology can be used such as the use of M13 for single stranded DNA as described by J. Messing (1983) Methods Enzymol, 101:20-78.

Other methods of oligonucleotide synthesis include phosphotriester and phosphodiester methods (Narang, *et al.* (1979) Meth. Enzymol 68:90) and synthesis on a support (Beaucage, *et al.* (1981) Tetrahedron Letters 22:1859-1862) as well as phosphoramidite techniques (Caruthers, M. H., *et al.*, "Methods in Enzymology," Vol. 154, pp. 287-314 (1988)) and others described in "Synthesis and Applications of DNA and RNA," S.A. Narang, editor, Academic Press, New York, 1987, and the references contained therein. The chemical synthesis via a photolithographic method of spatially addressable arrays of oligonucleotides bound to glass surfaces is described by A. C. Pease, *et al.*, Proc. Nat. Acad. Sci. USA (1994) 91:5022-5026.

Oligonucleotide probe -- an oligonucleotide employed to bind to a portion of a polynucleotide such as another oligonucleotide or a target nucleotide sequence.

The design and preparation of the oligonucleotide probes are generally dependent upon the sensitivity and specificity required, the sequence of the target polynucleotide and, in certain cases, the biological significance of certain portions of the target polynucleotide sequence.

- 5 Oligonucleotide primer(s) -- an oligonucleotide that is usually employed in a chain extension on a polynucleotide template such as in, for example, an amplification of a nucleic acid. The oligonucleotide primer is usually a synthetic nucleotide that is single stranded, containing a sequence at its 3'-end that is capable of hybridizing with a defined sequence of the target polynucleotide.
- 10 Normally, an oligonucleotide primer has at least 80%, preferably 90%, more preferably 95%, most preferably 100%, complementarity to a defined sequence or primer binding site. The number of nucleotides in the hybridizable sequence of an oligonucleotide primer should be such that stringency conditions used to hybridize the oligonucleotide primer will prevent excessive random non-specific
- 15 hybridization. Usually, the number of nucleotides in the oligonucleotide primer will be at least as great as the defined sequence of the target polynucleotide, namely, at least ten nucleotides, preferably at least 15 nucleotides, and generally from about 10 to 200, preferably 20 to 50, nucleotides.

- In general, in primer extension, amplification primers hybridize to, and are
- 20 extended along (chain extended), at least the target nucleotide sequence within the target polynucleotide and, thus, the target sequence acts as a template. The extended primers are chain "extension products." The target sequence usually lies between two defined sequences but need not. In general, the primers hybridize with the defined sequences or with at least a portion of such target
- 25 polynucleotide, usually at least a ten-nucleotide segment at the 3'-end thereof and preferably at least 15, frequently a 20 to 50 nucleotide segment thereof.

- Nucleoside triphosphates -- nucleosides having a 5'-triphosphate substituent. The nucleosides are pentose sugar derivatives of nitrogenous bases of either purine or pyrimidine derivation, covalently bonded to the 1'-carbon of the
- 30 pentose sugar, which is usually a deoxyribose or a ribose. The purine bases include adenine (A), guanine (G), inosine (I), and derivatives and analogs thereof. The pyrimidine bases include cytosine (C), thymine (T), uracil (U), and derivatives and analogs thereof. Nucleoside triphosphates include deoxyribonucleoside

triphosphates such as the four common deoxyribonucleoside triphosphates dATP, dCTP, dGTP and dTTP and ribonucleoside triphosphates such as the four common triphosphates rATP, rCTP, rGTP and rUTP.

The term "nucleoside triphosphates" also includes derivatives and analogs thereof, which are exemplified by those derivatives that are recognized and polymerized in a similar manner to the underivatized nucleoside triphosphates.

Nucleotide -- a base-sugar-phosphate combination that is the monomeric unit of nucleic acid polymers, i.e., DNA and RNA. The term "nucleotide" as used herein includes modified nucleotides as defined below.

DNA -- deoxyribonucleic acid.

RNA -- ribonucleic acid.

Modified nucleotide -- a unit in a nucleic acid polymer that contains a modified base, sugar or phosphate group. The modified nucleotide can be produced by a chemical modification of the nucleotide either as part of the nucleic acid polymer or prior to the incorporation of the modified nucleotide into the nucleic acid polymer. For example, the methods mentioned above for the synthesis of an oligonucleotide may be employed. In another approach a modified nucleotide can be produced by incorporating a modified nucleoside triphosphate into the polymer chain during an amplification reaction. Examples of modified nucleotides, by way of illustration and not limitation, include dideoxynucleotides, derivatives or analogs that are biotinylated, amine modified, alkylated, fluorophore-labeled, and the like and also include phosphorothioate, phosphite, ring atom modified derivatives, and so forth.

Nucleoside -- is a base-sugar combination or a nucleotide lacking a phosphate moiety.

Nucleotide polymerase -- a catalyst, usually an enzyme, for forming an extension of a polynucleotide along a DNA or RNA template where the extension is complementary thereto. The nucleotide polymerase is a template dependent polynucleotide polymerase and utilizes nucleoside triphosphates as building blocks for extending the 3'-end of a polynucleotide to provide a sequence complementary with the polynucleotide template. Usually, the catalysts are enzymes, such as DNA polymerases, for example, prokaryotic DNA polymerase (I, II, or III), T4 DNA polymerase, T7 DNA polymerase, Klenow fragment, reverse

transcriptase, Vent DNA polymerase, Pfu DNA polymerase, Taq DNA polymerase, and the like, or RNA polymerases, such as T3 and T7 RNA polymerases. Polymerase enzymes may be derived from any source such as cells, bacteria such as E. coli, plants, animals, virus, thermophilic bacteria, and so forth.

Amplification of nucleic acids or polynucleotides -- any method that results in the formation of one or more copies of a nucleic acid or polynucleotide molecule (exponential amplification) or in the formation of one or more copies of only the complement of a nucleic acid or polynucleotide molecule (linear amplification).

Hybridization (hybridizing) and binding -- in the context of nucleotide sequences these terms are used interchangeably herein. The ability of two nucleotide sequences to hybridize with each other is based on the degree of complementarity of the two nucleotide sequences, which in turn is based on the fraction of matched complementary nucleotide pairs. The more nucleotides in a given sequence that are complementary to another sequence, the more stringent the conditions can be for hybridization and the more specific will be the binding of the two sequences. Increased stringency is achieved by elevating the temperature, increasing the ratio of co-solvents, lowering the salt concentration, and the like.

Hybridization efficiency -- the productivity of a hybridization reaction, measured as either the absolute or relative yield of oligonucleotide probe/polynucleotide target duplex formed under a given set of conditions in a given amount of time.

Homologous or substantially identical polynucleotides -- In general, two polynucleotide sequences that are identical or can each hybridize to the same polynucleotide sequence are homologous. The two sequences are homologous or substantially identical where the sequences each have at least 90%, preferably 100%, of the same or analogous base sequence where thymine (T) and uracil (U) are considered the same. Thus, the ribonucleotides A, U, C and G are taken as analogous to the deoxynucleotides dA, dT, dC, and dG, respectively. Homologous sequences can both be DNA or one can be DNA and the other RNA.

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Complementary -- Two sequences are complementary when the sequence of one can bind to the sequence of the other in an anti-parallel sense wherein the 3'-end of each sequence binds to the 5'-end of the other sequence and each A, T(U), G, and C of one sequence is then aligned with a T(U), A, C, and G, respectively, of the other sequence. RNA sequences can also include complementary G/U or U/G basepairs.

Member of a specific binding pair ("sbp member") -- one of two different molecules, having an area on the surface or in a cavity that specifically binds to and is thereby defined as complementary with a particular spatial and polar organization of the other molecule. The members of the specific binding pair are referred to as cognates or as ligand and receptor (antiligand). These may be members of an immunological pair such as antigen-antibody, or may be operator-repressor, nuclease-nucleotide, biotin-avidin, hormones-hormone receptors, nucleic acid duplexes, IgG-protein A, DNA-DNA, DNA-RNA, and the like.

Ligand -- any compound for which a receptor naturally exists or can be prepared.

Receptor ("antiligand") -- any compound or composition capable of recognizing a particular spatial and polar organization of a molecule, e.g., epitope or determinant site. Illustrative receptors include naturally occurring receptors, e.g., thyroxine binding globulin, antibodies, enzymes, Fab fragments, lectins, nucleic acids, repressors, protection enzymes, protein A, complement component C1q, DNA binding proteins or ligands and the like.

#### Oligonucleotide Properties:

Potential of an oligonucleotide to hybridize -- the combination of duplex formation rate and duplex dissociation rate that determines the amount of duplex nucleic acid hybrid that will form under a given set of experimental conditions in a given amount of time.

Parameter -- a factor that provides information about the hybridization of an oligonucleotide with a target nucleotide sequence. Generally, the factor is one that is predictive of the ability of an oligonucleotide to hybridize with a target

nucleotide sequence. Such factors include composition factors, thermodynamic factors, chemosynthetic efficiencies, kinetic factors, and the like.

Parameter predictive of the ability to hybridize -- a parameter calculated from a set of oligonucleotide sequences wherein the parameter positively correlates with observed hybridization efficiencies of those sequences. The parameter is, therefore, predictive of the ability of those sequences to hybridize. "Positive correlation" can be rigorously defined in statistical terms. The correlation coefficient  $\rho_{x,y}$  of two experimentally measured discrete quantities  $x$  and  $y$  ( $N$  values in each set) is defined as

$$\rho_{x,y} = \frac{\text{Covariance}(x,y)}{\sqrt{\text{Variance}(x)\text{Variance}(y)}},$$

where the Covariance ( $x,y$ ) is defined by

$$\text{Covariance}(x,y) = \frac{1}{N} \sum_{j=1}^N (x_j - \mu_x)(y_j - \mu_y).$$

The quantities  $\mu_x$  and  $\mu_y$  are the averages of the quantities  $x$  and  $y$ , while the variances are simply the squares of the standard deviations (defined below). The correlation coefficient is a dimensionless (unitless) quantity between  $-1$  and  $1$ . A correlation coefficient of  $1$  or  $-1$  indicates that  $x$  and  $y$  have a linear relationship with a positive or negative slope, respectively. A correlation coefficient of zero indicates no relationship; for example, two sets of random numbers will yield a correlation coefficient near zero. Intermediate correlation coefficients indicate intermediate degrees of relatedness between two sets of numbers. The correlation coefficient is a good statistical measure of the degree to which one set of numbers predicts a second set of numbers.

Composition factor -- a numerical factor based solely on the composition or sequence of an oligonucleotide without involving additional parameters, such as experimentally measured nearest-neighbor thermodynamic parameters. For instance, the fraction  $(G+C)$ , given by the formula

$$f_{GC} = \frac{n_G + n_C}{n_G + n_C + n_A + n_{T \text{ or } U}},$$

where  $n_G$ ,  $n_C$ ,  $n_A$  and  $n_{T \text{ or } U}$  are the numbers of G, C, A and T (or U) bases in an oligonucleotide, is an example of a composition factor. Examples of composition factors, by way of illustration and not limitation, are mole fraction (G+C), percent (G+C), sequence complexity, sequence information content, frequency of occurrence of specific oligonucleotide sequences in a sequence database and so forth.

Thermodynamic factor -- numerical factors that predict the behavior of an oligonucleotide in some process that has reached equilibrium. For instance, the free energy of duplex formation between an oligonucleotide and its complement is a thermodynamic factor. Thermodynamic factors for systems that can be subdivided into constituent parts are often estimated by summing contributions from the constituent parts. Such an approach is used to calculate the thermodynamic properties of oligonucleotides.

Examples of thermodynamic factors, by way of illustration and not limitation, are predicted duplex melting temperature, predicted enthalpy of duplex formation, predicted entropy of duplex formation, free energy of duplex formation, predicted melting temperature of the most stable intramolecular structure of the oligonucleotide or its complement, predicted enthalpy of the most stable intramolecular structure of the oligonucleotide or its complement, predicted entropy of the most stable intramolecular structure of the oligonucleotide or its complement, predicted free energy of the most stable intramolecular structure of the oligonucleotide or its complement, predicted melting temperature of the most stable hairpin structure of the oligonucleotide or its complement, predicted enthalpy of the most stable hairpin structure of the oligonucleotide or its complement, predicted entropy of the most stable hairpin structure of the oligonucleotide or its complement, predicted free energy of the most stable hairpin structure of the oligonucleotide or its complement, thermodynamic partition function for intramolecular structure of the oligonucleotide or its complement and the like.

Chemosynthetic efficiency -- oligonucleotides and nucleotide sequences may both be made by sequential polymerization of the constituent nucleotides. However, the individual addition steps are not perfect; they instead proceed with some fractional efficiency that is less than unity. This may vary as a function of position in the sequence. Therefore, what is really produced is a family of molecules that consists of the desired molecule plus many truncated sequences. These "failure sequences" affect the observed efficiency of hybridization between an oligonucleotide and its complementary target. Examples of chemosynthetic efficiency factors, by way of illustration and not limitation, are coupling efficiencies, overall efficiencies of the synthesis of a target nucleotide sequence or an oligonucleotide probe, and so forth.

Kinetic factor -- numerical factors that predict the rate at which an oligonucleotide hybridizes to its complementary sequence or the rate at which the hybridized sequence dissociates from its complement are called kinetic factors. Examples of kinetic factors are steric factors calculated via molecular modeling or measured experimentally, rate constants calculated via molecular dynamics simulations, associative rate constants, dissociative rate constants, enthalpies of activation, entropies of activation, free energies of activation, and the like.

Predicted duplex melting temperature -- the temperature at which an oligonucleotide mixed with a hybridizable nucleotide sequence is predicted to form a duplex structure (double-helix hybrid) with 50% of the hybridizable sequence. At higher temperatures, the amount of duplex is less than 50%; at lower temperatures, the amount of duplex is greater than 50%. The melting temperature  $T_m$  (°C) is calculated from the enthalpy ( $\Delta H$ ), entropy ( $\Delta S$ ) and  $C$ , the concentration of the most abundant duplex component (for hybridization arrays, the soluble hybridization target), using the equation

$$T_m = \frac{\Delta H}{\Delta S + R \ln C} - 273.15,$$

where  $R$  is the gas constant, 1.987 cal/(mole·°K). For longer sequences (>100 nucleotides),  $T_m$  can also be estimated from the mole fraction ( $G+C$ ),  $\chi_{G+C}$ , using the equation

$$T_m = 81.5 + 41.0 \chi_{G+C}.$$

Melting temperature corrected for salt concentration -- polynucleotide duplex melting temperatures are calculated with the assumption that the concentration of sodium ion,  $Na^+$ , is 1 M. Melting temperatures  $T_m$  calculated for duplexes formed at different salt concentrations are corrected via the semi-empirical equation

$$T'_m([Na^+]) = T_m + 16.6 \log([Na^+]).$$

Predicted enthalpy, entropy and free energy of duplex formation -- the enthalpy ( $\Delta H$ ), entropy and free energy ( $\Delta G$ ) are thermodynamic state functions, related by the equation

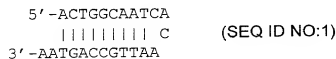
$$\Delta G = \Delta H - T \Delta S,$$

where  $T$  is the temperature in °K. In practice, the enthalpy and entropy are predicted via a thermodynamic model of duplex formation (the "nearest neighbor" model which is explained in more detail below), and used to calculate the free energy and melting temperature.

Predicted free energy of the most stable intramolecular structure of an oligonucleotide or its complement -- single-stranded DNA and RNA molecules that contain self-complementary sequences can form intramolecular secondary structures. For instance, the oligonucleotide

5' -ACTGGCAATCACAATTGCCAGTAA-3' (SEQ ID NO:1)

can base pair with itself, to form the structure



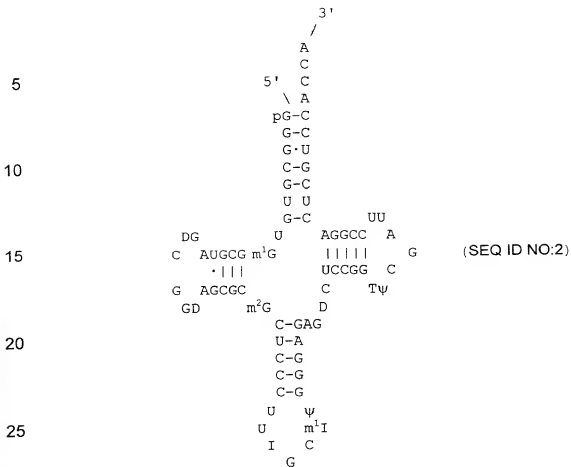
where a vertical line indicates Watson-Crick base pair formation. Many such structures are possible for a given sequence; two are of particular interest. The first is the lowest energy "hairpin" structure (formed by folding a sequence back on itself with a connecting loop at least 3 nucleotides long). The second is the lowest energy structure that can be formed by including more complex topologies, such as "bulge loops" (unpaired duplexes between two regions of base-paired duplex) and cloverleaf structures, where 3 base-paired stretches meet at a triple-junction. A good example of a complex secondary structure is the structure of a tRNA molecule, an example of which, namely, yeast tRNA<sup>Ala</sup> is shown below.

For either type of structure, a value of the free energy of that structure can be calculated, relative to the unpaired strand, by means of a thermodynamic model similar to that used to calculate the free energy of a base-paired duplex structure. Again, the free energy  $\Delta G$  is calculated from the enthalpy  $\Delta H$  and the entropy  $\Delta S$  at a given absolute temperature  $T$  via the equation

$$\Delta G = \Delta H - T \Delta S .$$

However, in this case there is the added difficulty that the lowest energy structure must be found. For a simple hairpin structure, this optimization can be performed via a relatively simple search algorithm. For more complex structures (such as a cloverleaf) a dynamic programming algorithm, such as that implemented in the program MFOLD, must be used.

Yeast tRNA<sup>Ala</sup> - The RNA sequence includes many non-standard ribonucleotides, such as D (5,6 dihydrouridine), m<sup>1</sup>G (1-methylguanosine), m<sup>2</sup>G (N<sup>2</sup>-dimethylguanosine),  $\psi$  (pseudouridine), I (inosine), m<sup>1</sup>I (1-methylinosine) and T (ribothymidine). Dots (·) mark (non-standard) G=U base pairs. The structure is taken from A. L. Lehninger, *et al.*, Principles of Biochemistry, 2<sup>nd</sup> Ed. (Worth Publishers, New York, NY, 1993).



Coupling efficiencies -- chemosynthetic efficiencies are called coupling efficiencies when the synthetic scheme involves successive attachment of different monomers to a growing oligomer; a good example is oligonucleotide synthesis via phosphoramidite coupling chemistry.

#### Algorithmic Operations:

Evaluating a parameter -- determination of the numerical value of a numerical descriptor of a property of an oligonucleotide sequence by means of a formula, algorithm or look-up table.

Filter -- a mathematical rule or formula that divides a set of numbers into two subsets. Generally, one subset is retained for further analysis while the other is discarded. If the division into two subsets is achieved by testing the numbers against a simple inequality, then the filter is referred to as a "cut-off". In the context of the current invention, an example by way of illustration and not limitation is the statement "The predicted self structure free energy must be

greater than or equal to  $-0.4$  kcal/mole," which can be used as a filter for oligonucleotide sequences; this particular filter is also an example of a cut-off.

Filter set -- A set of rules or formulae that successively winnow a set of numbers by identifying and discarding subsets that do not meet specific criteria. In the context of the current invention, an example by way of illustration and not limitation is the compound statement "the predicted self structure free energy must be greater than or equal to  $-0.4$  kcal/mole and the predicted RNA/DNA heteroduplex melting temperature must lie between  $60^{\circ}\text{C}$  and  $85^{\circ}\text{C}$ ," which can be used as a filter set for oligonucleotide sequences.

Examining a parameter -- comparing the numerical value of a parameter to some cutoff-value or filter.

Statistical sampling of a cluster -- extraction of a subset of oligonucleotides from a cluster of oligonucleotides based upon some statistical measure, such as rank by oligonucleotide starting position in the sequence complementary to the target sequence.

First quartile, median and third quartile -- If a set of numbers is ranked by value, then the value that divides the lower  $\frac{1}{4}$  from the upper  $\frac{3}{4}$  of the set is the first quartile, the value that divides the set in half is the median and the value that divides the lower  $\frac{3}{4}$  from the upper  $\frac{1}{4}$  of the set is the third quartile.

Poorly correlated -- If it is not possible to perform a "good" prediction, as defined via statistics, of one set of numbers from another set of numbers using a simple linear model, then the two sets of numbers are said to be poorly correlated.

Computer program -- a written set of instructions that symbolically instructs an appropriately configured computer to execute an algorithm that will yield desired outputs from some set of inputs. The instructions may be written in one or several standard programming languages, such as C, C++, Visual BASIC, FORTRAN or the like. Alternatively, the instructions may be written by imposing a template onto a general-purpose numerical analysis program, such as a spreadsheet.

#### Experimental System Components:

Small organic molecule -- a compound of molecular weight less than 1500, preferably 100 to 1000, more preferably 300 to 600 such as biotin, fluorescein,

achieve a consensus behavior. In other words, the oligonucleotide sequences should be sufficiently numerous that several possible probes overlap or fall within a given region that is expected to yield acceptable hybridization efficiency. Since the location of these regions is not known before hand, the best strategy is to

5 equally space the probe sequences along the sequence that is hybridizable to the target sequence. Since regions of acceptable hybridization efficiency are generally on the order of 20 nucleotides in length, a practical strategy is to space the starting nucleotides of the oligonucleotide sequences no more than five basepairs apart. If computation time needed to calculate the predictive

10 parameters is not an issue, then the best strategy is to space the starting nucleotides one nucleotide apart. An important feature of the present invention is to determine oligonucleotides that are clustered along a region of the nucleotide sequence. The individual predictions made for individual oligonucleotide sequences are not very good. However, we have found that the predictions that

15 are experimentally observed tend to form contiguous clusters, while the spurious predictions tend to be solitary. Thus, the number of oligonucleotides should be sufficient to achieve the desired clustering.

Preferably, a set of overlapping sequences is chosen. To this end, the subsequences are chosen so that there is overlap of at least one nucleotide from

20 one oligonucleotide to the next. More preferably, the overlap is two or more nucleotides. Most preferably, the oligonucleotides are spaced one nucleotide apart and the predetermined number is  $L-N+1$  oligonucleotides where L is the length of the nucleotide sequence and N is the length of the oligonucleotides. In the latter situation, the unique oligonucleotides are of identical length N. Thus, a

25 set of overlapping oligonucleotides is a set of oligonucleotides that are subsequences derived from some master sequence by subdividing that sequence in such a way that each subsequence contains either the start or end of at least one other subsequence in the set.

An example of the above for purposes of illustration and not limitation is presented by the sequence ATGGACTTAGCATTCG (SEQ ID NO:3), from which the following set of overlapping oligonucleotides can be identified:

ATGGACTTAGCA (SEQ ID NO:4)  
TGGACTTAGCAT (SEQ ID NO:5)  
GGACTTAGCATT (SEQ ID NO:6)  
GACTTAGCATTC (SEQ ID NO:7)  
ACTTAGCATTCG (SEQ ID NO:8)

In this example the overlapping oligonucleotides are spaced one nucleotide apart. In other words, there is overlap of all but one nucleotide from one oligonucleotide to the next. In the example above, the original nucleotide sequence is 16 nucleotides long (L=16). The length of each of the overlapping oligonucleotides is 12 nucleotides long (N=12) and there are  $L-N+1 = 5$  oligonucleotides.

The length of the oligonucleotides may be the same or different and may vary depending on the length of the nucleotide sequence. The length of the oligonucleotides is determined by a practical compromise between the limits of current chemistries for oligonucleotide synthesis and the need for longer oligonucleotides, which exhibit greater binding affinity for the target sequence and are more likely to occur only once in complicated mixtures of polynucleotide targets. Usually, the length of the oligonucleotides is from about 10 to 50 nucleotides, more usually, from about 25 to 35 nucleotides.

In the next step of the method at least one parameter that is independently predictive of the ability of each of the oligonucleotides of the set to hybridize to the target nucleotide sequence is determined and evaluated for each of the above oligonucleotides. Examples of such a parameter, by way of illustration and not limitation, is a parameter selected from the group consisting of composition factors, thermodynamic factors, chemosynthetic efficiencies, kinetic factors and mathematical combinations of these quantities.

The determination of a parameter may be carried out by known methods. For example, melting temperature of the oligonucleotide/target duplex may be determined using the nearest neighbor method and parameters appropriate for the nucleotide acids involved. For DNA/DNA parameters, see J. SantaLucia Jr., *et al.*, (1996) Biochemistry, 35:3555. For RNA/DNA parameters, see N. Sugimoto, *et al.*, (1995) Biochemistry, 34:11211. Briefly, these methods are

based on the observation that the thermodynamics of a nucleic acid duplex can be modeled as the sum of a term arising from the entire duplex and a set of terms arising from overlapping pairs of nucleotides ("nearest neighbor" model). For a discussion of the nearest neighbor see J. SantaLucia Jr., *et al.*, (1996)

- 5 Biochemistry, *supra*, and N. Sugimoto, *et al.*, (1995) Biochemistry, *supra*. For example, the enthalpy  $\Delta H$  of the duplex formed by the sequence

ATGGACTTAGCA (SEQ ID NO:4)

- 10 and its perfect complement can be approximated by the equation

$$\Delta H \cong H_{init} + H_{AT} + H_{TG} + H_{GG} + H_{GA} + H_{AC} \\ + H_{CT} + H_{TT} + H_{TA} + H_{AG} + H_{GC} + H_{CA} .$$

- 15 In the above equation, the term  $H_{init}$  is the initiation enthalpy for the entire duplex, while the terms  $H_{AT}$ , ...,  $H_{CA}$  are the so-called "nearest neighbor" enthalpies. Similar equations can be written for the entropy, for the corresponding quantities for RNA homoduplexes, or for DNA/RNA heteroduplexes. The free energy can then be calculated from the enthalpy, entropy and absolute temperature, as described previously.

- 20 Predicted free energy of the most stable intramolecular structure of an oligonucleotide ( $\Delta G_{MFOLD}$ ) may be determined using the nucleic acid folding algorithm MFOLD and parameters appropriate for the oligonucleotide, e.g., DNA or RNA. For MFOLD, see J.A. Jaeger, *et al.*, (1989), *supra*. For DNA folding parameters, see J. SantaLucia Jr., *et al.*, (1996), *supra*. Briefly, these methods  
25 operate in two steps. First, a map of all possible compatible intramolecular base pairs is made. Second, the global minimum of the free energy of the various possible base pairing configurations is found, using the nearest neighbor model to estimate the enthalpy and entropy, the user input temperature to complete the calculation of free energy, and a dynamic programming algorithm to find the global  
30 minimum. The algorithm is computationally intensive; calculation times scale as the third power of the sequence length.

The following Table 1 summarizes groups of parameters that are independently predictive of the ability of each of the oligonucleotides to hybridize to the target nucleotide sequence together with a reference to methods for their determination. Parameters within a given group are known or expected to be strongly correlated to one another, while parameters in different groups are known or expected to be poorly correlated with one another.

Table 1

| Group | Parameter   | Source or Reference   |
|-------|---|---|
| I     | duplex enthalpy, $\Delta H$                       | Santa Lucia <i>et al.</i> , 1996; Sugimoto <i>et al.</i> , 1995               |
|       | duplex entropy, $\Delta S$                        | Santa Lucia <i>et al.</i> , 1996; Sugimoto <i>et al.</i> , 1995               |
|       | duplex free energy, $\Delta G$                    | $\Delta G = \Delta H - T\Delta S$ (see text)                                  |
|       | melting temperature, $T_m$                        | (see text)  |
|       | mole fraction (or percent) G+C                    | self-explanatory  |
|       | subsequence duplex enthalpy                       | Santa Lucia <i>et al.</i> , 1996; Sugimoto <i>et al.</i> , 1995               |
|       | subsequence duplex entropy                        | Santa Lucia <i>et al.</i> , 1996; Sugimoto <i>et al.</i> , 1995               |
|       | subsequence duplex free energy                    | $\Delta G = \Delta H - T\Delta S$ (see text)                                  |
|       | subsequence duplex $T_m$                          | (see text)  |
|       | subsequence duplex mole fraction (or percent) G+C | self-explanatory  |
| II    | intramolecular enthalpy, $\Delta H_{MFOLD}$       | Jaeger <i>et al.</i> , 1989; Santa Lucia <i>et al.</i> , 1996                 |
|       | intramolecular entropy, $\Delta S_{MFOLD}$        | Jaeger <i>et al.</i> , 1989; Santa Lucia <i>et al.</i> , 1996                 |
|       | intramolecular free energy, $\Delta G_{MFOLD}$    | $\Delta G = \Delta H - T\Delta S$ (see text)                                  |
|       | hairpin enthalpy, $\Delta H_{hairpin}$            | Jaeger <i>et al.</i> , 1989; Santa Lucia <i>et al.</i> , 1996                 |
|       | hairpin entropy, $\Delta S_{hairpin}$             | Jaeger <i>et al.</i> , 1989; Santa Lucia <i>et al.</i> , 1996                 |
|       | hairpin free energy, $\Delta G_{hairpin}$         | $\Delta G = \Delta H - T\Delta S$ (see text)                                  |
|       | intramolecular partition function, $Z$            | $Z = \sum_{k \text{ structures}} \exp(-\Delta G_{intramolecular}^{(k)} / RT)$ |
| III   | sequence complexity                               | Altschul <i>et al.</i> , 1994   |
|       | sequence information content                      | Altschul <i>et al.</i> , 1994   |
| IV    | steric factors                                    | molecular modeling or experiment  |
|       | molecular dynamic simulation                      | Weber & Hefland, 1979   |
|       | enthalpy, entropy & free energy of activation     | measured experimentally   |
| V     | association & dissociation rates                  | Patzel & Sczakiel, 1998   |
|       | oligonucleotide chemosynthetic efficiencies       | measured experimentally   |
| VI    | target synthetic efficiencies                     | measured experimentally   |

In a next step of the present method, a subset of oligonucleotides within the predetermined number of unique oligonucleotides is identified based on the above evaluation of the parameter. A number of mathematical approaches may be followed to sort the oligonucleotides based on a parameter. In one approach a cut-off value is established. The cut-off value is adjustable and can be optimized

relative to one or more training data sets. This is done by first establishing some metric for how well a cutoff value is performing; for example, one might use the normalized signal observed for each oligonucleotide in the training set. Once such a metric is established, the cutoff value can be numerically optimized to maximize the value of that metric, using optimization algorithms well known to the art. Alternatively, the cutoff value can be estimated using graphical methods, by graphing the value of the metric as a function of one or more parameters, and then establishing cutoff values that bracket the region of the graph where the chosen metric exceeds some chosen threshold value. In essence, the cut off values are chosen so that the rule set used yields training data that maximizes the inclusion of oligonucleotides that exhibit good hybridization efficiency and minimizes the inclusion of oligonucleotides that exhibit poor hybridization efficiency.

A preferred approach to performing such a graph-based optimization of filter parameters is shown in Fig. 3. In Fig. 3, hybridization data from several different genes have been used to prepare a contour plot of relative hybridization intensity as a function of DNA/RNA heteroduplex melting temperature and free energy of the most stable intramolecular structure of the probe. Contours are shown only for regions for which there are data; the white space outside of the outermost contour indicates that there are no experimental data for that region. The details of how the data were obtained can be found in Example 1 below. A summary of the sequences and number of data points employed is shown in Table 2 below. The measured hybridization intensities for each data set were normalized prior to construction of the contour plot depicted in Fig. 3 by dividing each observed intensity by the maximum intensity observed for that gene. In addition, differences in hybridization salt concentrations and hybridization temperatures were accounted for by using the salt concentration-corrected values of the melting temperatures and by subtracting the hybridization temperature from each predicted melting temperature, respectively. The filter set determined by examination of Fig. 3 is indicated by both the dotted open box in the figure and by the inequalities above the box.

One way in which such a contour plot may be prepared involves the use of an appropriate software application such as Microsoft® Excel® or the like. For

example, the cross-tabulation tool may be used in the Microsoft® Excel® program. Data is accumulated into rectangular bins that are 0.5 kcal  $\Delta G_{MFOLD}$  wide and 2.5°C  $T_m$  wide. In each bin the average values of  $\Delta G_{MFOLD}$ ,  $T_m - T_{hyb}$ , and the normalized hybridization intensity are calculated. The data is output to the software application DeltaGraph® (Deltapoint, Inc., Monterey, CA) and the contour plot is prepared using the tools and instructions provided.

Table 2

| Target (GenBank Accession No.)                                     | Target Strand | No. Data Points | $T_{hyb}$ | [Na <sup>+</sup> ] Correction |
|--|---------------|-----------------|-----------|-------------------------------|
| HIV protease-reverse transcriptase (PRT) <sup>a</sup> (M15654)     | Sense         | 1,022           | 35°C      | -1.4°C                        |
| HIV protease-reverse transcriptase (PRT) <sup>a</sup> (M15654)     | antisense     | 1,041           | 30°C      | -1.4°C                        |
| HIV protease-reverse transcriptase (PRT) <sup>b</sup> (M15654)     | Sense         | 88              | 35°C      | -1.4°C                        |
| Human G3PDH (glyceraldehyde-3-dehydrogenase) <sup>b</sup> (X01677) | antisense     | 93              | 35°C      | -1.4°C                        |
| Human p53 <sup>c</sup> (X02469)                                    | antisense     | 93              | 35°C      | -1.4°C                        |
| Rabbit $\beta$ -globin <sup>c</sup> (K03256)                       | antisense     | 106             | 30°C      | 0°C                           |

<sup>a</sup> Data from Affymetrix GeneChip™ Array

<sup>b</sup> Data from biotinylated probes bound to streptavidin-coated microtiter wells

<sup>c</sup> Literature data: see N. Milner, K. U. Mir & E. M. Southern (1997) *Nature Biotech.* **15**, 537-541.

Once the cut-off value is selected, a subset of oligonucleotides having parameter values greater than or equal to the cut-off value is identified. This refers to the inclusion of oligonucleotides in a subset based on whether the value of a predictive parameter satisfies an inequality.

Examples of identifying a subset of oligonucleotides by establishing cut-off values for predictive parameters are as follows: for melting temperature an inequality might be  $60^\circ\text{C} \leq T_m$ ; for predicted free energy an inequality, preferably, might be

$$\Delta G_{MFOLD} \geq -0.4 \frac{\text{kcal}}{\text{mole}}.$$

In a variation of the above, both a maximum and a minimum cut-off value may be selected. A subset of oligonucleotides is identified whose values fall

within the maximum and minimum values, i.e., values greater than or equal to the minimum cut-off value and less than or equal to the maximum cut-off value. An example of this approach for melting temperature might be the inequality  $60^{\circ}\text{C} \leq T_m \leq 85^{\circ}\text{C}$ .

With regard to cut off values for  $T_m$  the lower limit is most important, and is preferably  $T_m = T_{hyb}$ , more preferably,  $T_m = T_{hyb} + 15^{\circ}\text{C}$ . The upper cutoff is important when the sequence region under consideration is unusually rich in G and C, and is preferably  $T_m = T_{hyb} + 40^{\circ}\text{C}$ . With regard to  $\Delta G_{MFOLD}$  the cutoff value is usually greater than or equal to  $-1.0$  kcal/mole. As mentioned above, the cutoff values preferably are determined from real data through experimental observations.

In another approach the parameter values may be converted into dimensionless numbers. The parameter value is converted into a dimensionless number by determining a dimensionless score for each parameter resulting in a distribution of scores having a mean value of zero and a standard deviation of one. The dimensionless score is a number that is used to rank some object (such as an oligonucleotide) to which that score relates. A score that has no units (i.e., a pure number) is called a dimensionless score.

In one approach the following equations are used for converting the values of said parameters into dimensionless numbers:

$$s_{i,x} = \frac{x_i - \langle x \rangle}{\sigma_{\{x\}}},$$

where  $s_{i,x}$  is the dimensionless score derived from parameter  $x$  calculated for oligonucleotide  $i$ ,  $x_i$  is the value of parameter  $x$  calculated for oligonucleotide  $i$ ,  $\langle x \rangle$  is the average of parameter  $x$  calculated for all of the oligonucleotides under consideration for a given nucleotide sequence target, and  $\sigma_{\{x\}}$  is the standard deviation of parameter  $x$  calculated for all of the oligonucleotides under consideration for a given nucleotide sequence target, and is given by the equation

$$\sigma_{\{x\}} = \sqrt{\frac{\sum_{j=1}^M (x_j - \langle x \rangle)^2}{M-1}},$$

where M is the number of oligonucleotides. The resulting distribution of scores,  $\{s\}$  has a mean value of zero and a standard deviation of one. These properties

5 can be important for a combination of the scores discussed below.

The use of a dimensionless number approach may further include calculating a combination score  $S_i$  by evaluating a weighted average of the individual values of the dimensionless scores  $s_{i,x}$  by the equation:

$$10 \quad S_i = \sum_{\{x\}} q_x s_{i,x},$$

where  $q_x$  is the weight assigned to the score derived from parameter x, the individual values of  $q_x$  are always greater than zero, and the sum of the weights  $q_x$  is unity.

15 In another variation of the above approach, the method of calculation of the composite parameter is optimized based on the correlation of the individual composite scores to real data, as explained more fully below.

In one approach the calculation of the composite score further involves determining a moving window-averaged combination score  $\langle S_i \rangle$  for the  $i$ th probe  
20 by the equation:

$$\langle S_i \rangle = \frac{1}{w} \sum_{j=i-\frac{w-1}{2}}^{i+\frac{w-1}{2}} S_j, \quad w = \text{an odd integer},$$

where w is the length of the window for averaging (i.e., w nucleotides long), and then applying a cutoff filter to the value of  $\langle S_i \rangle$ . This procedure results in  
25 smoothing (smoothing procedure) by turning each score into a consensus metric for a set of w adjacent oligonucleotide probes. The score, referred to as the "smoothed score," is essentially continuous rather than a few discrete values. The

value of the smoothed score is strongly influenced by clustering of scores with high or low values; window averaging therefore provides a measurement of cluster size.

An advantage of the dimensionless score approach to the probe prediction algorithm is that it is easy to objectively optimize. In one approach to training the algorithm, optimization of the weights  $q_x$  above may be performed by varying the values of the weights so that the correlation coefficient  $\rho_{\{<S_i>\},\{V_j\}}$  between the set of window-averaged combination scores  $\{<S_i>\}$  and a set of calibration experimental measurements  $\{V_j\}$  is maximized. The correlation coefficient  $\rho_{\{<S_i>\},\{V_j\}}$  is calculated from the equation

$$\rho_{\{<S_i>\},\{V_j\}} = \left( \frac{1}{M} \right) \frac{\text{Covariance}(\langle S \rangle, V)}{\sigma_{\{<S_i>\}} \sigma_{\{V_j\}}},$$

where  $M$  is the number of window averaged, combination dimensionless scores and the number of corresponding measurements, the covariance is as defined earlier (see earlier equations) and  $\sigma_{\{<S_i>\}}$  and  $\sigma_{\{V_j\}}$  are the standard deviations of  $\{<S_i>\}$  and  $\{V_j\}$ , as defined previously. An example of this approach is shown in Example 2, below.

In another approach the parameter is derived from one or more factors by mathematical transformation of the factors. This involves the calculation of a new predictive parameter from one or more existing predictive parameters, by means of an equation. For instance, the equilibrium constant  $K_{open}$  for formation of an oligonucleotide with no intramolecular structure from its structured form can be calculated from the intramolecular structure free energy  $\Delta G_{MFOLD}$ , using the equation:

$$K_{open} = \exp\left(\frac{\Delta G_{MFOLD}}{RT}\right).$$

In a next step of the method oligonucleotides in the subset are then identified that are clustered along a region of the nucleotide sequence that is

hybridizable to the target nucleotide sequence. For example, consider a set of overlapping oligonucleotides identified by dividing a nucleotide sequence into subsequences. A subset of the oligonucleotides is obtained as described above. In general, this subset is obtained by applying a rule that rejects some members of the set. For the remaining members of the set, namely, the subset, there will be some average number of nucleotides in the nucleotide sequence between the first nucleotides of adjacent remaining subsequences. If, for some sub-region of the nucleotide sequence, the average number of nucleotides in the nucleotide sequence between the first nucleotides of adjacent remaining subsequences is less than the average for the entire nucleotide sequence, then the oligonucleotides are clustered. The smaller the average number of nucleotides between the first nucleotides of adjacent oligonucleotides, the stronger the clustering. The strongest clustering occurs when there are no intervening nucleotides between adjacent starting nucleotides. In this case, the oligonucleotides are said to be contiguous and may be referred to as contiguous sequence elements or "contigs."

Accordingly, in this step oligonucleotides are sorted based on length of contiguous sequence elements. Oligonucleotides in the subset determined above are identified that are contiguous along a region of the input nucleic acid sequence. The length of each contig that is equal to the number of oligonucleotides in each contig, namely, oligonucleotides from the above step whose complement begin at positions  $m+1$ ,  $m+2$ , ...,  $m+k$  in the target sequence, form a contig of length  $k$ . Contigs can be identified and contig length can be calculated using, for example, a Visual Basic® module that can be incorporated into a Microsoft® Excel workbook.

Cluster size can be defined in several ways:

For contiguous clusters, the size is simply the number of adjacent oligonucleotides in the cluster. Again, this may also be referred to as contiguous sequence elements. The number may also be referred to as "contig length". For example, consider the nucleotide sequence discussed above, namely, ATGGACTTAGCATTCG (SEQ ID NO:3) and the identified set of overlapping oligonucleotides

rhodamine and other dyes, tetracycline and other protein binding molecules, and haptens, *etc.* The small organic molecule can provide a means for attachment of a nucleotide sequence to a label or to a support.

Support or surface -- a porous or non-porous water insoluble material. The surface can have any one of a number of shapes, such as strip, plate, disk, rod, particle, including bead, and the like. The support can be hydrophilic or capable of being rendered hydrophilic and includes inorganic powders such as glass, silica, magnesium sulfate, and alumina; natural polymeric materials, particularly cellulosic materials and materials derived from cellulose, such as fiber containing papers, e.g., filter paper, chromatographic paper, etc.; synthetic or modified naturally occurring polymers, such as nitrocellulose, cellulose acetate, poly (vinyl chloride), polyacrylamide, cross linked dextran, agarose, polyacrylate, polyethylene, polypropylene, poly(4-methylbutene), polystyrene, polymethacrylate, poly(ethylene terephthalate), nylon, poly(vinyl butyrate), etc.; either used by themselves or in conjunction with other materials; glass available as Bioglass, ceramics, metals, and the like. Natural or synthetic assemblies such as liposomes, phospholipid vesicles, and cells can also be employed.

Binding of oligonucleotides to a support or surface may be accomplished by well-known techniques, commonly available in the literature. See, for example, A. C. Pease, *et al.*, Proc. Nat. Acad. Sci. USA, 91:5022-5026 (1994).

Label -- a member of a signal producing system. Usually the label is part of a target nucleotide sequence or an oligonucleotide probe, either being conjugated thereto or otherwise bound thereto or associated therewith. The label is capable of being detected directly or indirectly. Labels include (i) reporter molecules that can be detected directly by virtue of generating a signal, (ii) specific binding pair members that may be detected indirectly by subsequent binding to a cognate that contains a reporter molecule, (iii) oligonucleotide primers that can provide a template for amplification or ligation or (iv) a specific polynucleotide sequence or recognition sequence that can act as a ligand such as for a repressor protein, wherein in the latter two instances the oligonucleotide primer or repressor protein will have, or be capable of having, a reporter molecule. In general, any reporter molecule that is detectable can be used.

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The reporter molecule can be isotopic or nonisotopic, usually non-isotopic, and can be a catalyst, such as an enzyme, a polynucleotide coding for a catalyst, promoter, dye, fluorescent molecule, chemiluminescent molecule, coenzyme, enzyme substrate, radioactive group, a small organic molecule, amplifiable polynucleotide sequence, a particle such as latex or carbon particle, metal sol, crystallite, liposome, cell, etc., which may or may not be further labeled with a dye, catalyst or other detectable group, and the like. The reporter molecule can be a fluorescent group such as fluorescein, a chemiluminescent group such as luminol, a terbium chelator such as N-(hydroxyethyl) ethylenediaminetriacetic acid that is capable of detection by delayed fluorescence, and the like.

The label is a member of a signal producing system and can generate a detectable signal either alone or together with other members of the signal producing system. As mentioned above, a reporter molecule can be bound directly to a nucleotide sequence or can become bound thereto by being bound to an sbp member complementary to an sbp member that is bound to a nucleotide sequence. Examples of particular labels or reporter molecules and their detection can be found in U.S. Patent No. 5,508,178 issued April 16, 1996, at column 11, line 66, to column 14, line 33, the relevant disclosure of which is incorporated herein by reference. When a reporter molecule is not conjugated to a nucleotide sequence, the reporter molecule may be bound to an sbp member complementary to an sbp member that is bound to or part of a nucleotide sequence.

Signal Producing System -- the signal producing system may have one or more components, at least one component being the label. The signal producing system generates a signal that relates to the presence or amount of a target polynucleotide in a medium. The signal producing system includes all of the reagents required to produce a measurable signal. Other components of the signal producing system may be included in a developer solution and can include substrates, enhancers, activators, chemiluminescent compounds, cofactors, inhibitors, scavengers, metal ions, specific binding substances required for binding of signal generating substances, and the like. Other components of the signal producing system may be coenzymes, substances that react with enzymic products, other enzymes and catalysts, and the like. The signal producing system

provides a signal detectable by external means, by use of electromagnetic radiation, desirably by visual examination. Signal-producing systems that may be employed in the present invention are those described more fully in U.S. Patent No. 5,508,178, the relevant disclosure of which is incorporated herein by reference.

Ancillary Materials -- Various ancillary materials will frequently be employed in the methods and assays utilizing oligonucleotide probes designed in accordance with the present invention. For example, buffers and salts will normally be present in an assay medium, as well as stabilizers for the assay medium and the assay components. Frequently, in addition to these additives, proteins may be included, such as albumins, organic solvents such as formamide, quaternary ammonium salts, polycations such as spermine, surfactants, particularly non-ionic surfactants, binding enhancers, e.g., polyalkylene glycols, or the like.

#### DETAILED DESCRIPTION OF THE INVENTION

The invention is directed to methods or algorithms for predicting oligonucleotides specific for a nucleic acid target where the oligonucleotides exhibit a high potential for hybridization. The algorithm uses parameters of the oligonucleotide and the oligonucleotide/target nucleotide sequence duplex, which can be readily predicted from the primary sequences of the target polynucleotide and candidate oligonucleotides. In the methods of the present invention, oligonucleotides are filtered based on one or more of these parameters, then further filtered based on the sizes of clusters of oligonucleotides along the input polynucleotide sequence. The methods or algorithms of the present invention may be carried out using either relatively simple user-written subroutines or publicly available stand-alone software applications (e.g., dynamic programming algorithm for calculating self-structure free energies of oligonucleotides). The parameter calculations may be orchestrated and the filtering algorithms may be implemented using any of a number of commercially available computer programs as a framework such as, e.g., Microsoft® Excel spreadsheet, Microsoft® Access relational database and the like. The basic steps involved in the present methods involve parsing a sequence that is complementary to a target nucleotide sequence into a set of overlapping oligonucleotide sequences, evaluating one or more

parameters for each of the oligonucleotide sequences, said parameter or parameters being predictive of probe hybridization to the target nucleotide sequence, filtering the oligonucleotide sequences based on the values for each parameter, filtering the oligonucleotide sequences based on the length of contiguous sequence elements and ranking the contiguous sequence elements based on their length. We have found that oligonucleotides in the longest contiguous sequence elements generally show the highest hybridization efficiencies.

The present methods are based on our recognition that oligonucleotides showing high hybridization efficiencies tend to form clusters. It is believed that this clustering reflects local regions of the target nucleotide sequence that are unstructured and accessible for oligonucleotide binding. Oligonucleotides that are contiguous along a region of the input nucleic acid sequence are identified. These oligonucleotides are sorted based on the length of the contiguous sequence elements. The sorting approach used in the present invention apparently serves as a surrogate for the calculation of local secondary structure of the target nucleotide sequence. This is supported by our observation that treatments intended to eliminate long-range nucleic acid structure (e.g., random fragmentation) do not eliminate the differences in hybridization yields across oligonucleotide probe arrays. This implies that major determinants of efficient hybridization are local regions of the target sequence. The identification of contiguous sequence elements is a simple and efficient method for recognizing clusters of such determinants and, thus, for identifying oligonucleotide probes that exhibit high hybridization efficiency for a target nucleotide sequence.

As mentioned above one embodiment of the present invention is a method for predicting the potential of an oligonucleotide to hybridize to a target nucleotide sequence. A predetermined number of unique oligonucleotides is identified. The length of the oligonucleotides may be the same or different. The oligonucleotides are unique in that no two of the oligonucleotides are identical. The unique oligonucleotides are chosen to sample the entire length of a nucleotide sequence that is hybridizable with the target nucleotide sequence. The actual number of oligonucleotides is generally determined by the length of the nucleotide sequence and the desired result. The number of oligonucleotides should be sufficient to

- ATGGACTTAGCA (SEQ ID NO:4)  
 TGGACTTAGCAT (SEQ ID NO:5)  
 GGACTTAGCATT (SEQ ID NO:6)  
 GACTTAGCATTC (SEQ ID NO:7)  
 5     ACTTAGCATTCG (SEQ ID NO:8)

Suppose that, after calculation and evaluation of the predictive parameters, four nucleotides remain:

- |    |              |               |  |                        |
|----|--------------|---------------|--|------------------------|
| 10 | ATGGACTTAGCA | (SEQ ID NO:4) |  | contig                 |
|    | TGGACTTAGCAT | (SEQ ID NO:5) |  |                        |
|    | GGACTTAGCATT | (SEQ ID NO:6) |  |                        |
|    | ACTTAGCATTCG | (SEQ ID NO:8) |  | single oligonucleotide |

- 15 A "contig" encompassing three of the oligonucleotides of the subset is present together with a single oligonucleotide. The contig length is 3 oligonucleotides.

- Alternatively, cluster size at some position in the sequence hybridizable or complementary to the target sequence may be defined as the number of oligonucleotides whose center nucleotides fall inside a region of length M centered about the position in question, divided by M. This definition of clustering allows small gaps in clusters. In the example used above for contiguous clusters, if M was 10, then the cluster size would step through the values 0/10,..., 0/10, 1/10, 2/10, 3/10, 3/10, 4/10, 4/10, 4/10, 4/10, 3/10, 2/10, 1/10, 0/10 as the center of the window of length 10 passed through the cluster. In each fraction,
- 20 the numerator is the number of oligonucleotide sequences that have satisfied the filter set and whose central nucleotides are within a window 10 nucleotides long, centered about the nucleotide under consideration. The denominator (10) is simply the window length.
- 25

- Another alternative is to define the size of a cluster at some position in the sequence hybridizable or complementary to the target sequence as the number of oligonucleotide sequences overlapping that position. This definition is equivalent to the last definition with M set equal to the oligonucleotide probe length and omission of the division by M.
- 30

- Finally, cluster size can be approximated at each position in a nucleotide sequence by dividing the sequence into oligonucleotides, evaluating a numerical score for each oligonucleotide, and then averaging the scores in the neighborhood
- 35

of each position by means of a moving window average as described above. Window averaging has the effect of reinforcing clusters of high or low values around a particular position, while canceling varying values about that position. The window average, therefore, provides a score that is sensitive to both the

- 5 hybridization potential of a given oligonucleotide and the hybridization potentials of its neighbors.

- In a next step of the present method, the oligonucleotides in the subset are ranked. Generally, this ranking is based on the lengths of the clusters or contigs, sizes of the clusters or values of a window averaged score. Oligonucleotides  
10 found in the longest contigs or largest clusters, or possessing the highest window averaged scores usually show the highest hybridization efficiencies. Often, the highest signal intensity within the cluster corresponds to the median oligonucleotide of the cluster. However, the peak signal intensity within the contig can be determined experimentally, by sampling the cluster at its first quartile,  
15 midpoint and third quartile, measuring the hybridization efficiencies of the sampled oligonucleotides, interpolating or extrapolating the results, predicting the position of the optimal probe, and then iterating the probe design process.

- Fig. 1 shows a diagram of an example of the above-described method by way of illustration and not limitation. Referring to Fig. 1 a target sequence of  
20 length L from, e.g., a database, is used to generate a sequence that is hybridizable to the target sequence from which candidate oligonucleotide probe sequences are generated. One or more parameters are calculated for each of the oligonucleotide probe sequences. The candidate oligonucleotide probe sequences are filtered based on the values of the parameters. Clustering of the  
25 filtered candidate probe sequences is evaluated and the clusters are ranked by size. Then, the oligonucleotide probes are statistically sampled and synthesized. Further evaluation may be made by evaluating the hybridization of the selected oligonucleotide probes in real hybridization experiments. The above process may be reiterated to further define the selection. In this way only a small fraction of the  
30 potential oligonucleotide probe candidates are synthesized and tested. This is in sharp contrast to the known method of synthesizing and testing all or a major portion of potential oligonucleotide probes for a given target sequence.

The methods of the present invention are preferably carried out at least in part with the aid of a computer. For example, an IBM® compatible personal computer (PC) may be utilized. The computer is driven by software specific to the methods described herein.

5 The preferred computer hardware capable of assisting in the operation of the methods in accordance with the present invention involves a system with at least the following specifications: Pentium® processor or better with a clock speed of at least 100 MHz, at least 32 megabytes of random access memory (RAM) and at least 80 megabytes of virtual memory, running under either the Windows 95 or  
10 Windows NT 4.0 operating system (or successor thereof).

As mentioned above, software that may be used to carry out the methods may be either Microsoft Excel or Microsoft Access, suitably extended via user-written functions and templates, and linked when necessary to stand-alone programs that calculate specific parameters (e.g., MFOLD for intramolecular  
15 thermodynamic parameters). Examples of software programs used in assisting in conducting the present methods may be written, preferably, in Visual BASIC, FORTRAN and C++, as exemplified below in the Examples. It should be understood that the above computer information and the software used herein are by way of example and not limitation. The present methods may be adapted to  
20 other computers and software. Other languages that may be used include, for example, PASCAL, PERL or assembly language.

Fig. 2 depicts a more specific approach to a method in accordance with the present invention. Referring to Fig. 2, a sequence of length L is obtained from a database such as GenBank, UniGene or a proprietary sequence database. Probe  
25 length N is determined by the user based on the requirements for sensitivity and specificity and the limitations of the oligonucleotide synthetic scheme employed. The probe length and sequence length are used to generate L-N+1 candidate oligonucleotide probes, i.e., from every possible starting position. An initial selection is made based on local sequence predicted thermodynamic properties.  
30 To this end, melting temperature  $T_m$  and the self-structure free energy  $\Delta G_{MFOLD}$ , are calculated for each of the potential oligonucleotide probe: target nucleotide sequence complexes. Next, M probes that satisfy  $T_m$  and  $\Delta G_{MFOLD}$  filters are selected. A further selection can be made based on clustering of "good"

parameters. Good parameters are parameters that satisfy all of the filters in the filter set. Clustering is defined by any of the methods described previously; in Fig. 2, the "contig length" definition of clustering is used.

For each of the M oligonucleotide sequences that satisfied all filters the question is asked whether the oligonucleotide sequence immediately following the sequence under consideration is also one of the sequences that satisfied all of the filters. If the answer to this question is NO, then one stores the current value of the contig length counter, resets the counter to zero and proceeds to the next oligonucleotide sequence that satisfied all filters. If the answer to the question is YES, then 1 is added to the contig length counter and, if the counter now equals 1 (i.e., this is the first oligonucleotide probe sequence in the contig), the starting position of the oligonucleotide is stored. One then moves to the next oligonucleotide that satisfied all filters, which, in this case, is the same as the next oligonucleotide before the application of the filter set. The process is repeated until all M filtered oligonucleotide sequences have been examined. In this way, a single pass through the set of M filtered oligonucleotide sequences generates the lengths and starting positions of all contigs.

Next, contigs are ranked based on the lengths of their contiguous sequence elements. Longer contig lengths generally correlate with higher hybridization efficiencies. All oligonucleotides of the higher-ranking contigs may be considered, or candidate oligonucleotide probes may be picked. For example, candidate oligonucleotide probes can be picked one quarter, one half and three quarters of the way through each contig. The latter approach provides local curvature determination after experimental determination of hybridization efficiencies, which allows either interpolation or extrapolation of the positions of the next probes to be synthesized in order to close in on the optimal probe in the region. If the contig brackets the actual peak of hybridization efficiency, the process will converge in 2-3 iterations. If the contig lies to one side of the actual peak, the process will converge in 3-4 iterations.

The above illustrative approach is further described with reference to the following DNA nucleotide sequence, which is the complement of the target RNA nucleotide sequence:

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GTCCAAAAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA  
(SEQ ID NO:9).

In the first step of the method, the nucleotide sequence is divided into overlapping oligonucleotides that are 25 nucleotides in length. This length is chosen because  
5 it is an effective compromise between the need for sensitivity (enhanced by longer oligonucleotides) and the chemosynthetic efficiency of schemes for synthesis of surface-bound arrays of oligonucleotide probes.

Next, the estimated duplex melting temperatures ( $T_m$ ) and self-structure  
10 free energies ( $\Delta G_{MFOLD}$ ) are calculated for each oligonucleotide in the set of overlapping oligonucleotides. The values are obtained from a user-written function that calculates DNA/RNA heteroduplex thermodynamic parameters (see N. Sugimoto, *et al.*, Biochemistry, 34:11211 (1995)) and a modified version of the program MFOLD that estimates the free energy of the most stable intramolecular

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structure of a single stranded DNA molecule (see J.A. Jaeger, *et al.*, (1989), *supra*, respectively. The steps are illustrated below.

|    |  |  |
|----|--|--|
| 5  | GTCCAAAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA | (target complement sequence)             |
|    |  |  |
|    | GTCCAAAAGGGTCAGTCTACCTCC                         | T <sub>m</sub> (°C) ΔG <sub>M</sub> FOLD |
|    | TCCAAAAGGGTCAGTCTACCTCCC                         | 71.77 -1.20 SEQ ID NO:10                 |
| 10 | CCAAAAGGGTCAGTCTACCTCCCG                         | 71.99 -1.20 SEQ ID NO:11                 |
|    | CAAAAAGGGTCAGTCTACCTCCCGC                        | 70.78 -1.20 SEQ ID NO:12                 |
|    | AAAAAGGGTCAGTCTACCTCCCGCC                        | 71.23 -1.20 SEQ ID NO:13                 |
|    | AAAAGGGTCAGTCTACCTCCGCCA                         | 73.07 -1.20 SEQ ID NO:14                 |
|    | AAAGGGTCAGTCTACCTCCGCCAT                         | 75.68 -1.20 SEQ ID NO:15                 |
| 15 | AAGGGTCAGTCTACCTCCCGCCATA                        | 77.53 -1.20 SEQ ID NO:16                 |
|    | AGGGTCAGTCTACCTCCCGCCATAA                        | 79.03 -1.20 SEQ ID NO:17                 |
|    | GGGTCAGTCTACCTCCCGCCATAAA                        | 79.03 -1.20 SEQ ID NO:18                 |
|    | GGTCAGTCTACCTCCCGCCATAAAA                        | 76.85 -1.20 SEQ ID NO:19                 |
|    | GTCACTCTACCTCCCGCCATAAAAA                        | 73.10 -0.80 SEQ ID NO:20                 |
| 20 | TCACTCTACCTCCCGCCATAAAAAA                        | 69.50 0.90 SEQ ID NO:21                  |
|    | CAGTCTACCTCCCGCCATAAAAAAC                        | 65.60 0.90 SEQ ID NO:22                  |
|    | AGTCTACCTCCCGCCATAAAAAACT                        | 64.96 0.90 SEQ ID NO:23                  |
|    | GTCTACCTCCCGCCATAAAAAACTC                        | 65. 1.10 SEQ ID NO:24                    |
| 25 | TCTACCTCCCGCCATAAAAAACTCA                        | 66.36 2.40 SEQ ID NO:25                  |
|    | CTACCTCCCGCCATAAAAAACTCAT                        | 64.97 2.90 SEQ ID NO:26                  |
|    | TACCTCCCGCCATAAAAAACTCATG                        | 63.96 2.70 SEQ ID NO:27                  |
|    | ACCTCCCGCCATAAAAAACTCATGT                        | 62.58 1.10 SEQ ID NO:28                  |
|    | CCTCCCGCCATAAAAAACTCATGTT                        | 65.10 0.40 SEQ ID NO:29                  |
| 30 | CTCCCGCCATAAAAAACTCATGTTCA                       | 64.96 0.10 SEQ ID NO:30                  |
|    | TCCCGCCATAAAAAACTCATGTTCAA                       | 63.37 -0.10 SEQ ID NO:31                 |
|    | CCCGCCATAAAAAACTCATGTTCAA                        | 62.86 -0.10 SEQ ID NO:32                 |
|    | CCGCCATAAAAAACTCATGTTCAAG                        | 60.47 -0.10 SEQ ID NO:33                 |
|    | CGCCATAAAAAACTCATGTTCAAGA                        | 57.98 -0.10 SEQ ID NO:34                 |
| 35 |  | 56.20 -0.10 SEQ ID NO:35                 |

Next, the oligonucleotide sequences are filtered on the basis of  $T_m$ . A high and low cut-off value may be selected, for example,  $60^\circ\text{C} \leq T_m \leq 85^\circ\text{C}$ . Thus, oligonucleotides having  $T_m$  values falling within the above range are retained. Those outside the range are discarded, which is indicated below by lining out of those oligonucleotides and parameter values.

GTCCAAAAGGGTCAGTCTACCTCCGCCATAAAAACTCATGTTCAAGA (target complement sequence)

|    |                            | $T_m$ ( $^\circ\text{C}$ ) | $\Delta G_{\text{MFOLD}}$ |
|----|----------------------------|----------------------------|---------------------------|
| 10 | GTCCAAAAGGGTCAGTCTACCTCC   | 71.77                      | -1.20                     |
|    | TCCAAAAGGGTCAGTCTACCTCCC   | 71.99                      | -1.20                     |
|    | CCAAAAGGGTCAGTCTACCTCCCG   | 70.78                      | -1.20                     |
|    | CAAAAAGGGTCAGTCTACCTCCGCG  | 71.23                      | -1.20                     |
| 15 | AAAAAGGGTCAGTCTACCTCCGCGC  | 73.07                      | -1.20                     |
|    | AAAAAGGGTCAGTCTACCTCCGCGCA | 75.68                      | -1.20                     |
|    | AAAGGGTCAGTCTACCTCCGCGCAT  | 77.53                      | -1.20                     |
|    | AAGGGTCAGTCTACCTCCGCGCATA  | 79.03                      | -1.20                     |
|    | AGGGTCAGTCTACCTCCGCGCCATAA | 79.03                      | -1.20                     |
| 20 | GGGTCAGTCTACCTCCGCGCCATAAA | 76.85                      | -1.20                     |
|    | GGTCAGTCTACCTCCGCGCCATAAAA | 73.10                      | -0.80                     |
|    | GTCAGTCTACCTCCGCGCCATAAAAA | 69.50                      | 0.90                      |
|    | TCAGTCTACCTCCGCGCCATAAAAAA | 65.60                      | 0.90                      |
|    | CAGTCTACCTCCGCGCCATAAAAAAC | 64.96                      | 0.90                      |
| 25 | AGTCTACCTCCGCGCCATAAAAAACT | 65.48                      | 1.10                      |
|    | GTCTACCTCCGCGCCATAAAAAACTC | 66.36                      | 2.40                      |
|    | TCTACCTCCGCGCCATAAAAAACTCA | 64.97                      | 2.90                      |
|    | CTACCTCCGCGCCATAAAAAACTCAT | 63.96                      | 2.70                      |
|    | TACCTCCGCGCCATAAAAAACTCATG | 62.58                      | 1.10                      |
| 30 | ACCTCCGCGCCATAAAAAACTCATGT | 65.10                      | 0.40                      |
|    | CCTCCGCGCCATAAAAAACTCATGTT | 64.96                      | 0.10                      |
|    | CTCCGCGCCATAAAAAACTCATGTTC | 63.37                      | -0.10                     |
|    | TCCGCGCCATAAAAAACTCATGTTCA | 62.86                      | -0.10                     |
|    | CCGCGCCATAAAAAACTCATGTTCAA | 60.47                      | -0.10                     |
| 35 | GGCGCCATAAAAAACTCATGTTCAAG | 57.98                      | -0.10                     |
|    | GGCCTAAAAAACTCATGTTCAAGA   | 56.29                      | -0.10                     |

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Next, the oligonucleotide sequences remaining after the above exercise are filtered on the basis of  $\Delta G_{MFOLD}$  and are retained if the value is greater than - 0.4. Those oligonucleotides with a  $\Delta G_{MFOLD}$  less than - 0.4 are discarded, which is indicated below by double lining out of those oligonucleotides and parameter values.

GTCCAAAAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA (target complement sequence)

10

|    |  | $T_m$ (°C) | $\Delta G_{MFOLD}$ |
|----|--|------------|--------------------|
|    | <del>GTCCAAAAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA</del> | 71.77      | <del>-1.30</del>   |
|    | <del>GTCCAAAAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA</del> | 71.99      | <del>-1.30</del>   |
|    | <del>GTCCAAAAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA</del> | 70.78      | <del>-1.30</del>   |
| 15 | <del>GTCCAAAAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA</del> | 71.23      | <del>-1.30</del>   |
|    | <del>GTCCAAAAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA</del> | 73.07      | <del>-1.30</del>   |
|    | <del>GTCCAAAAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA</del> | 75.68      | <del>-1.30</del>   |
|    | <del>GTCCAAAAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA</del> | 77.53      | <del>-1.30</del>   |
| 20 | <del>GTCCAAAAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA</del> | 79.03      | <del>-1.30</del>   |
|    | <del>GTCCAAAAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA</del> | 79.03      | <del>-1.30</del>   |
|    | <del>GTCCAAAAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA</del> | 76.85      | <del>-1.30</del>   |
|    | <del>GTCCAAAAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA</del> | 73.10      | <del>-0.90</del>   |
|    | GTCCAAAAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA            | 69.50      | 0.90               |
|    | GTCCAAAAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA            | 65.60      | 0.90               |
| 25 | GTCCAAAAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA            | 64.96      | 0.90               |
|    | GTCCAAAAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA            | 65.48      | 1.10               |
|    | GTCCAAAAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA            | 66.36      | 2.40               |
|    | GTCCAAAAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA            | 64.97      | 2.90               |
| 30 | GTCCAAAAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA            | 63.96      | 2.70               |
|    | GTCCAAAAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA            | 62.58      | 1.10               |
|    | GTCCAAAAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA            | 65.10      | 0.40               |
|    | GTCCAAAAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA            | 64.96      | 0.10               |
|    | GTCCAAAAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA            | 63.37      | -0.10              |
|    | GTCCAAAAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA            | 62.86      | -0.10              |
| 35 | GTCCAAAAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA            | 60.47      | -0.10              |
|    | GTCCAAAAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA            | 67.98      | -0.10              |
|    | GTCCAAAAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA            | 66.20      | -0.10              |

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- Clusters of retained oligonucleotides are identified and ranked based on cluster size. In this example, a contiguous cluster of 13 retained oligonucleotides is identified by the vertical black bar on the left. Any or all of the oligonucleotides in this cluster may be evaluated experimentally.

GTCCAAAAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA (target complement sequence)

|    |   | $T_m$ (°C) | $\Delta G_{MFOLD}$ |
|----|---|------------|--------------------|
| 10 | GTCCAAAAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA | 71.77      | -3.00              |
|    | GTCCAAAAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA | 71.99      | -3.00              |
|    | GTCCAAAAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA | 70.78      | -3.00              |
|    | GTCCAAAAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA | 71.23      | -3.00              |
| 15 | GTCCAAAAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA | 73.07      | -3.00              |
|    | GTCCAAAAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA | 75.68      | -3.00              |
|    | GTCCAAAAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA | 77.53      | -3.00              |
|    | GTCCAAAAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA | 79.03      | -3.00              |
| 20 | GTCCAAAAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA | 79.03      | -3.00              |
|    | GTCCAAAAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA | 76.85      | -3.00              |
|    | GTCCAAAAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA | 73.10      | -0.00              |
|    | GTCCAAAAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA | 69.50      | 0.90               |
|    | GTCCAAAAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA | 65.60      | 0.90               |
|    | GTCCAAAAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA | 64.96      | 0.90               |
| 25 | GTCCAAAAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA | 65.48      | 1.10               |
|    | GTCCAAAAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA | 66.36      | 2.40               |
|    | GTCCAAAAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA | 64.97      | 2.90               |
|    | GTCCAAAAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA | 63.96      | 2.70               |
|    | GTCCAAAAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA | 62.58      | 1.10               |
| 30 | GTCCAAAAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA | 65.10      | 0.40               |
|    | GTCCAAAAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA | 64.96      | 0.10               |
|    | GTCCAAAAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA | 63.37      | -0.10              |
|    | GTCCAAAAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA | 62.86      | -0.10              |
|    | GTCCAAAAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA | 60.47      | -0.10              |
| 35 | GTCCAAAAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA | 57.99      | -0.10              |
|    | GTCCAAAAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA | 56.29      | -0.10              |

Alternatively, in one approach the oligonucleotides at the first quartile, the median and the third quartile of the cluster may be selected for experimental evaluation, indicated below by bold print.

5

GTCCAAAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA (target complement sequence)

|    |  | $T_m$ (°C) | $\Delta G_{MFOLD}$ |
|----|--|------------|--------------------|
| 10 | GTCCAAAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA | 71.77      | -3.40              |
|    | TCCAAAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA  | 71.99      | -3.40              |
|    | GCAAAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA   | 70.78      | -3.40              |
|    | CAAAAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA   | 71.23      | -3.40              |
|    | AAAAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA    | 73.07      | -3.40              |
| 15 | AAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA      | 75.68      | -3.40              |
|    | AAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA      | 77.53      | -3.40              |
|    | AAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA      | 79.03      | -3.40              |
|    | AAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA      | 79.03      | -3.40              |
|    | AAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA      | 76.85      | -3.40              |
| 20 | AAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA      | 73.10      | -0.00              |
|    | GTCCAAAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA | 69.50      | 0.90               |
|    | TCCAAAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA  | 65.60      | 0.90               |
|    | GCAAAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA   | 64.96      | 0.90               |
|    | CAAAAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA   | 65.48      | 1.10               |
| 25 | AAAAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA    | 66.36      | 2.40               |
|    | AAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA      | 64.97      | 2.90               |
|    | AAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA      | 63.96      | 2.70               |
|    | AAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA      | 62.58      | 1.10               |
|    | AAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA      | 65.10      | 0.40               |
| 30 | AAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA      | 64.96      | 0.10               |
|    | AAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA      | 63.37      | -0.10              |
|    | AAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA      | 62.86      | -0.10              |
|    | AAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA      | 60.47      | -0.10              |
|    | AAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA      | 57.98      | -0.10              |
| 35 | AAAGGGTCAGTCTACCTCCCGCCATAAAAACTCATGTTCAAGA      | 56.20      | -0.10              |

In one aspect of the present method, at least two parameters are determined wherein the parameters are poorly correlated with respect to one another. The reason for requiring that the different parameters chosen are poorly correlated with one another is that an additional parameter that is strongly correlated to the original parameter brings no additional information to the prediction process. The correlation to the original parameter is a strong indication that both parameters represent the same physical property of the system. Another way of stating this is that correlated parameters are linearly dependent on one another, while poorly correlated parameters are linearly independent of one another. In practice, the absolute value of the correlation coefficient between any two parameters should be less than 0.5, more preferably, less than 0.25, and, most preferably, as close to zero as possible.

In one preferred approach instead of  $T_m$ , for each oligonucleotide/target nucleotide sequence duplex, the difference between the predicted duplex melting temperature corrected for salt concentration and the temperature of hybridization of each of the oligonucleotides with the target nucleotide sequence is determined.

5 In one aspect the present method comprises determining two parameters at least one of the parameters being the association free energy between a subsequence within each of the oligonucleotides and its complementary sequence on the target nucleotide sequence, or some similar, strongly correlated parameter. The object of this approach is to identify a particularly stable subsequence of the  
10 oligonucleotide that might be capable of acting as a nucleation site for the beginning of the heteroduplex formation between the oligonucleotide and the target nucleotide sequence. Such nucleation is believed to be the rate-limiting step for process of heteroduplex formation.

The subsequence within the oligonucleotide is from about 3 to 9  
15 nucleotides in length, usually, 5 to 7 nucleotides in length. The subsequence is at least three nucleotides from the terminus of the oligonucleotide. For support-bound oligonucleotides the subsequence is at least three nucleotides from the free end of the oligonucleotide, i.e., the end that is not attached to the support. Generally, this free end is the 5' end of the oligonucleotide. When the  
20 oligonucleotide is attached to a support, the subsequence is at least three nucleotides from the end of the oligonucleotide that is bound to the surface of the support to which the oligonucleotide is attached. Generally, the 3' end of the oligonucleotide is bound to the support.

The predictive parameter can be, for example, either melting temperature  
25 or duplex free energy of the subsequence with the target nucleotide sequence. The subsequence with the maximum (melting temperature) or minimum (free energy) value of one of the above parameters is chosen as the representative subsequence for that oligonucleotide probe. For example, if the oligonucleotide is 20 nucleotides in length and a subsequence of 5 nucleotides is chosen, i.e., a 5-  
30 mer, then parameter values are calculated for all 5-mer subsequences of the oligonucleotide that do not include the 2 nucleotides at the free end of the oligonucleotide. Where 5' is the free end of the oligonucleotide with designated nucleotide number 1, the values are calculated for all 5-mer subsequences with

starting nucleotides from position number 3 to position number 16. Thus, in this example, parameter values for 14 different subsequences are calculated. The subsequence with the maximum value for the parameter is then assigned as the stability subsequence for the oligonucleotide.

5           The inclusion of the above determination of a stability subsequence results in the following algorithm for determining the potential of an oligonucleotide to hybridize to a target nucleotide sequence. A predetermined number of unique oligonucleotides are identified within a nucleotide sequence that is hybridizable with said target nucleotide sequence. The oligonucleotides are chosen to sample  
10 the entire length of the nucleotide sequence. For each of the oligonucleotides, parameters that are independently predictive of the ability of each of said oligonucleotides to hybridize to said target nucleotide sequence are determined and evaluated. Two parameters that may be used are the thermodynamic parameters of  $T_m$  and  $\Delta G_{MFOLD}$ . These parameters give rise to associated  
15 parameter filters. In one approach evaluation of the parameters involves establishing cut-off values as described above. Application of these cut-off values results in the identification of a subset of oligonucleotides for further scrutiny under the algorithm. In accordance with this embodiment of the present invention, there is included a stability subsequence limit in addition to the above. Cutoff values  
20 are determined either by means of objective optimization algorithms well known to the art or via graphical estimation methods; both approaches have been described previously in this document. In either case, the optimization of cutoff values involves comparison of predictions to known hybridization efficiency data sets. This process results in objective optimization as it looks at prediction versus  
25 experimental results and is otherwise referred to herein as "training the algorithm." The experimental data used to train the algorithm is referred to herein as "training data."

In the present approach filters are assigned to the  $T_m$  oligonucleotide probe data. The  $T_m$  of each oligonucleotide probe needs to be greater than or equal to  
30 the assigned filter ( $T_m$  probe limit) to be given a filter score of "1"; otherwise, the filter score is "0". In addition, one can also impose a second filter for this parameter; that is, that the  $T_m$  of the oligonucleotide probe also has to be less than a defined upper limit. Filters are also assigned to the  $\Delta G_{MFOLD}$  data. The

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$\Delta G_{\text{MFOLD}}$  of each oligonucleotide probe should be greater than or equal to the assigned filter ( $\Delta G_{\text{MFOLD}}$  limit) to be given a filter score of "1"; otherwise, the filter score is "0". The filter scores are added. Furthermore, one can also impose a second filter for this parameter; that is, that the  $\Delta G_{\text{MFOLD}}$  also has to be less than a defined upper limit. In accordance with the above discussion stability subsequences are identified. This leads to another filter. Accordingly, filters are assigned to the stability sequence data. The stability subsequence of each oligonucleotide probe needs to be greater than or equal to the assigned filter limit to be given a filter score of "1"; otherwise, the filter score is "0". In addition, one can also impose a second filter for this parameter; that is, that the stability subsequence also has to be less than a defined upper limit. In all cases, the filter values are determined by objective optimization (algorithmic or graphical) of the predictions of the present method versus training data, as described previously.

On the basis of the above filter sets a subset of oligonucleotides within said predetermined number of unique oligonucleotides is identified. Oligonucleotides in the subset are identified that are clustered along a region of the nucleotide sequence that is hybridizable to the target nucleotide sequence. The resulting number of oligonucleotide probe regions is examined. The above filters may then be loosened or tightened by changing the filter limits to obtain more or fewer clusters of oligonucleotides to match the goal, which is set by the needs of the investigator. For instance, a particular application might require that the investigator design 5 non-overlapping probes that efficiently hybridize to a given target sequence.

As mentioned above, the contigs may be selected on the basis of contig length. In another approach, the scores defined above may be summed for cluster size determination. To this end the probe score of the particular filter set (e.g.,  $T_m$  probe limit,  $\Delta G_{\text{MFOLD}}$  limit and stability sequence limit) is calculated for each oligonucleotide probe. The probe score is the sum of the filter scores. Thus, the probe score is 0 if no parameters pass their respective filters. The probe score is 1, 2 or 3 if one, two or three parameters, respectively, pass their filters for that oligonucleotide probe. This summing is continued for each parameter that is in the current filter set of the algorithm used. For a given algorithm a minimum probe score limit is set. In the current example this limit will be at least 1 and could be 2

or 3 depending on the needs of the investigator, the number of probe clusters required and the results of objective optimizations of algorithm performance against training data. The probe score is compared to this probe score limit. If the probe score of oligonucleotide probe  $i$  is greater than or equal to the probe score limit, then oligonucleotide probe  $i$  is assigned a score passed value of 1. Next, a window is chosen for the evaluation of clustering (the "cluster window"). This will be the next filter applied. The cluster window (" $w$ ") smoothes the score passed values by summing the values in a window  $w$  nucleotides long, centered about position  $i$ . The resulting sum is called the cluster sum. Usually, the cluster window is an odd integer, usually 7 or 9 nucleotides. The cluster sum values are then filtered, by comparing to a user-set threshold, cluster filter. If cluster sum is greater than or equal to cluster filter, this filter is passed, and the probe is predicted to hybridize efficiently to its target.

This window summing procedure converts the score for the passed value for each oligonucleotide into a consensus metric for a set of  $w$  adjacent probes. A "consensus metric" is a measurement that distills a number of values into one consensus value. In this case, the consensus value is calculated by simply summing the individual values. The window summing procedure therefore evaluates a property similar to the contig length metric discussed above. However, the summed score has the advantage of allowing for a few probes within a cluster to have not passed their individual probe score limits. We have found that this allows more observed hybridization peaks to be predicted.

It may be desired in some circumstances to combine the results of multiple algorithm versions. We refer to this operation as "tiling". This may be explained more fully as follows. Tiling generally involves joining together the predicted oligonucleotide probe sets identified by multiple algorithm versions. In the context of the present invention, tiling multiple algorithm versions involves forming the union of multiple sets of predictions. These predictions may arise from different embodiments of the present invention. Alternatively, the different sets of predictions may arise from the same embodiment, but different filter sets. The different filter sets may additionally be restricted to different combinations of parameter values. For instance, one filter set might be used when the predicted

duplex melting temperature  $T_m$  is greater than or equal to some value, while another might be used when  $T_m$  is below that value.

An example of the logical endpoint of tiling multiple filter sets across different regions of the possible combinations of predictive parameters and then forming the union of the resulting predictions is the contour plot shown in Fig. 3, with the associated rule that "the value of the normalized hybridization intensity associated with a particular combination of ( $T_m$ - $T_{hyb}$ ) and  $\Delta G_{MFOLD}$  must be greater than or equal to some threshold value." In this case, the contour at the threshold value becomes the filter. This contour and its interior can be thought of as the union of many small rectangular regions ("tiles"), each of which is bracketed by low and high cutoff values for each of the parameters.

The predictions of different algorithm versions can also be combined by forming the intersection of two or more different predictions. The reliability of predictions within such intersection sets is enhanced because such sets are, by definition, insensitive to changes in the details of the predictive algorithm. Intersection is a useful method for reducing the number of predicted probes when a single algorithm version produces too many candidate probes for efficient experimental evaluation.

The most specific oligonucleotide probe set (i.e., the set least likely to include poor probes) will be the intersection set from multiple algorithms. Clusters that have overlapping oligonucleotide probes from multiple algorithms constitute the intersection set of oligonucleotide probes. The oligonucleotide probe that is in the center of an intersection cluster is chosen. This central oligonucleotide probe may have the highest probability of predicting a peak or, in other words, of binding well to the target nucleotide sequence. Oligonucleotide probes on either side of center, which are still within the intersection cluster, may also be selected. The distance of these "side" oligonucleotide probes from the center generally will be shorter or longer depending upon the length of the cluster.

The most sensitive set of oligonucleotide probes (i.e., the set most likely to include at least one good probe) is generally the union set from multiple algorithms. Clusters that are predicted by at least one type of algorithm constitute the union set of oligonucleotide probes. The oligonucleotide probe in the center of a union cluster is chosen. Oligonucleotide probes on either side of center, which

are still within the union cluster, usually are also chosen. The distance of these side probes from the center will be shorter or longer depending upon the length of the cluster. In summary, the combination of using the stability subsequence parameter, tiling multiple filter sets, and making union and intersection cluster sets of oligonucleotide probes exhibits very high sensitivity and specificity in predicting oligonucleotide probes that effectively hybridize to a target nucleotide sequence of interest.

Another aspect of the present invention is a computer based method for predicting the potential of an oligonucleotide to hybridize to a target nucleotide sequence. A predetermined number of unique oligonucleotides within a nucleotide sequence that is hybridizable with the target nucleotide sequence is identified under computer control. The oligonucleotides are chosen to sample the entire length of the nucleotide sequence. A value is determined and evaluated under computer control for each of the oligonucleotides for at least one parameter that is independently predictive of the ability of each of the oligonucleotides to hybridize to the target nucleotide sequence. The parameter values are stored. Based on the examination of the stored parameter values, a subset of oligonucleotides within the predetermined number of unique oligonucleotides is identified under computer control. Then, oligonucleotides in the subset that are clustered along a region of the nucleotide sequence that is hybridizable to the target nucleotide sequence are identified under computer control.

A computer program is utilized to carry out the above method steps. The computer program provides for input of a target-hybridizable or target-complementary nucleotide sequence, efficient algorithms for computation of oligonucleotide sequences and their associated predictive parameters, efficient, versatile mechanisms for filtering sets of oligonucleotide sequences based on parameter values, mechanisms for computation of the size of clusters of oligonucleotide sequences that pass multiple filters, and mechanisms for outputting the final predictions of the method of the present invention in a versatile, machine-readable or human-readable form.

Another aspect of the present invention is a computer system for conducting a method for predicting the potential of an oligonucleotide to hybridize to a target nucleotide sequence. An input means for introducing a target

nucleotide sequence into the computer system is provided. The input means may permit manual input of the target nucleotide sequence. The input means may also be a database or a standard format file such as GenBank. Also included in the system is means for determining a number of unique oligonucleotide sequences that are within a nucleotide sequence that is hybridizable with the target nucleotide sequence. The oligonucleotide sequences is chosen to sample the entire length of the nucleotide sequence. Suitable means is a computer program or software, which also provides memory means for storing the oligonucleotide sequences. The system also includes means for controlling the computer system to carry out a determination and evaluation for each of the oligonucleotide sequences a value for at least one parameter that is independently predictive of the ability of each of the oligonucleotide sequences to hybridize to the target nucleotide sequence. Suitable means is a computer program or software such as, for example, Microsoft® Excel spreadsheet, Microsoft® Access relational database or the like, which also provides memory means for storing the parameter values. The system further comprises means for controlling the computer to carry out an identification of a subset of oligonucleotide sequences within the number of unique oligonucleotide sequences based on the automated examination of the stored parameter values. Suitable means is a computer program or software, which also allocates memory means for storing the subset of oligonucleotides. The system also includes means for controlling the computer to carry out an identification of oligonucleotide sequences in the subset that are clustered along a region of the nucleotide sequence that is hybridizable to the target nucleotide sequence. Suitable means is a computer program or software, which also allocates memory means for storing the oligonucleotide sequences in the subset. The computer system also includes means for outputting data relating to the oligonucleotide sequences in the subset. Such means may be machine readable or human readable and may be software that communicates with a printer, electronic mail, another computer program, and the like. One particularly attractive feature of the present invention is that the outputting means may communicate directly with software that is part of an oligonucleotide synthesizer. In this way the results of the method of the present invention may be used directly to provide instruction for the synthesis of the desired oligonucleotides.

Another advantage of the present invention is that it may be used to predict efficient hybridization oligonucleotides for each of multiple target sequences. Thus, very large arrays may be constructed and tested with minimal synthesis of oligonucleotides.

5

### EXAMPLES

The invention is demonstrated further by the following illustrative examples. Parts and percentages are by weight unless otherwise indicated. Temperatures are in degrees Centigrade (°C) unless otherwise specified. The following preparations and examples illustrate the invention but are not intended to limit its scope. All reagents used herein were from Amresco, Inc., Solon, Ohio (buffers), Pharmacia Biotech, Piscataway, N.J. (nucleoside triphosphates) or Promega, Madison, Wisconsin (RNA polymerases) unless indicated otherwise.

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#### Example 1

Synopsis: Data from labeled RNA target hybridizations to surface-bound DNA probes directed against 4 different gene sequences were compared to the predictions of the preferred version of the prediction algorithm illustrated by the flow chart in Fig. 2. The RNA targets were sequences derived from the human immunodeficiency virus protease-reverse transcriptase region (HIV PRT; sense-strand target polynucleotide), human glyceraldehyde-3-phosphate dehydrogenase gene (G3PDH; antisense-strand target polynucleotide), human tumor suppressor p53 gene (p53; antisense-strand target polynucleotide) and rabbit  $\beta$ -globin gene ( $\beta$ -globin; antisense-strand target polynucleotide). The GenBank accession numbers for the gene sequences, number of data points collected and temperature of hybridization have all been previously listed in Table 2.

20

25

Materials and Methods: Three different experimental systems and two different labeling schemes were used to collect data.

30

The sequence and hybridization data for  $\beta$ -globin were taken from the literature (see Milner *et al.*, (1997), *supra*; in this experiment,  $^{32}\text{P}$ -radiolabeled RNA target was used.

The hybridization data for HIV PRT were obtained using an Affymetrix GeneChip™ HIV PRT-sense probe array (i.e. sense strand target polynucleotide) (GeneChip™ HIV PRT 440s, Affymetrix Corporation, Santa Clara, California) as specified by the manufacturer, except that the fluorescein-labeled RNA target was not fragmented prior to hybridization and that hybridization was performed for 24 hours. The concentration of fluorescein-labeled RNA used was 26.3 nM; label density was approximately 18 fluoresceinated uridyl nucleotides per 1 kilobase (kb) RNA transcript. The raw data were collected by scanning the array with a GeneChip™ Scanner 50 (Affymetrix Corporation, Santa Clara, California), as specified by the manufacturer. The raw data were reduced to a feature-averaged (".CEL") file, using the GeneChip™ software supplied with the scanner. Finally, a table of hybridization intensities for perfect-complement 20-mer probes was constructed using the ASCII feature map file supplied with the GeneChip™ software to connect probe sequences to measured hybridization intensities. The resulting data set contained data for every overlapping 20-mer probe to the target sequence.

The data for G3PDH and p53 were measured using 93-feature arrays constructed using commercially available streptavidin-coated microtiter plates (Pierce Chemical Company, Rockford, IL). Every tenth possible 25-mer probe complementary to each target was synthesized and 3'-biotinylated by a contract synthesis vendor (Operon, Inc., Alameda, CA). The 3'-linked biotin was used to anchor individual probes to microtiter wells, via the well known, strong affinity of streptavidin for biotin. Biotinylated DNA probes were resuspended to a concentration of 10  $\mu\text{M}$  in hybridization buffer (5x sodium chloride-sodium phosphate-disodium ethylenediaminetetraacetate (SSPE), 0.05% Triton X-100, filter-sterilized; 1x SSPE is 150 mM sodium chloride, 10 mM sodium phosphate, 1 mM disodium ethylenediaminetetraacetate (EDTA), pH 7.4). Individual probes were diluted 1:10 in hybridization buffer into specified wells (100  $\mu\text{l}$  total volume per well) of a streptavidin-coated microtiter plate; probes were allowed to bind to the covered plates overnight at 35°C. The other 3 wells of the 96-well microtiter

plate were probe-less controls. The coated plates were washed with 3 x 200 µl of wash buffer (6x SSPE, 0.005% Triton X-100, filter-sterilized). Fluorescein-labeled RNA (100 µl of a 10 nM solution in hybridization buffer) was added to each well. The plates were covered and hybridized at 35°C for 20-24 hours. The hybridized plates were washed with 3 x 200 µl of wash buffer. Label was then released in each well by adding 100 µl of 20 µg/ml RNAase I (Sigma Chemical Company, St. Louis, MO) in Tris-EDTA (TE) (10 mM Tris(hydroxymethyl)aminomethane (Tris), 1 mM EDTA, pH 8.0, sterile) and incubating at 35°C for at least 30 minutes. The fluorescence released from the surface of each well was quantitated with a PerSeptive Biosystems Cytofluor II microtiter plate fluorimeter (PerSeptive Biosystems, Inc., Framingham, MA) using the manufacturer's recommended excitation and emission filter sets for fluorescein. Each plate hybridization was performed in quadruplicate, and the data for each probe were averaged to obtain the hybridization intensity.

Labeled RNA targets specific for G3PDH and p53 were produced via T7 RNA polymerase transcription of DNA templates in the presence of fluorescein-UTP (Boehringer Mannheim Corporation, Indianapolis, IN), using the same method as that outlined by Affymetrix for their GeneChip™ HIV PRT sense probe array. The DNA template for G3PDH was purchased from a commercial source (Clontech, Inc., Palo Alto, CA). The DNA template for p53 was obtained by sub-cloning a PCR fragment from an ATCC-derived reference clone (No. 57254) of human p53 into the commercially-available PCR cloning vector pCR2.1-TOPO (Invitrogen, Inc., Carlsbad, CA), then linearizing the plasmid at the end of the polycloning site opposite the vector-derived T7 promoter.

Probe predictions were performed using a software application (referred to as "p5") that was built atop Microsoft's Access relational database application, using added Visual Basic modules, the TrueDB Grid Pro 5.0 (Apex Software Corporation, Pittsburgh, PA) enhancement to Visual Basic, and a version of the FORTRAN application MFOLD, modified to run in a Windows NT 4.0 environment, as an ActiveX control. The Visual Basic source code for the p5 software application is found in the Microfiche appendix to this specification. The DNA target sequence complements that were input into p5 for division into potential oligonucleotide probe sequences are listed below:

Parent Sequence Accession No.: K03256

Locus: BUNGLOB.DNA (portion of rabbit  $\beta$  -globin)

Length: 122

5 1 TTCTTCCACA TTCACCTTGC CCCACAGGGC AGTGACCGCA GACTTCTCCT CACTGGACAG  
61 ATGCACCATT CTGTCTGTCT TGGGGGATTG CAAGTAAACA CAGTTGTGTC AAAAGCAAGT  
121 GT SEQ ID NO:36

Parent Sequence Accession No.: M15654

Locus: HIV PRTA.S (HIV PRT antisense; parses into probes specific for sense-strand target)

Length: 1040

10 1 TGTACTGTCC ATTTATCAGG ATGGAGTTCA TAACCCATCC AAAGGAATGG AGGTTCTTTT  
15 61 TGAATGTTTT TGTCGGTGT GGTAACTGCC CACCTCAACA GATGTTGTCT CAGCTCCCTCT  
121 ATTTTGTGTC TATGCTGCCC TATTTCTAAG TCAGATCCTA CATACAAATC ATCCATGTAT  
181 TGATAGATAA CTATGCTGCG ATTTTGTGTT TTAAAGAGCT CTAAGATTTT TGTCATGCTA  
241 CTTTGGAAATA TTGCTGGTGA TCCTTTCCAT CCCTGTGGAA GCACATTGTA CTGATATCTA  
301 ATCCCTGGTG TCTCATTGTT TATACTAGGT ATGGTAAATG CAGTATACTT CCTGAAGTCT  
20 361 TCATCTAAGG GAACTGAAAA ATATGCATCA CCCACATCCA GTACTGTTAC TGATTTTTTC  
421 TTTTTTAAAC CTGCGGGGATG TGGTATTCCT AATTGAACCT CCAGAGAGTC TTGAGTTCTC  
481 TTATTAAAGT CTCTGAAATC TACTAATTTT CTCCATTTAG TACTGTCTTT TTCTCTTATG  
541 GCAATACTCG GAGTATTGTA TGGATTCTCA GGCCCAATTT TTGAATTTT CCCTTCCCTT  
601 TCCATTTCCTG TACAATTTT TACTAATGCT TTTATTTTTT CTCTGTCAAA TGGCCATTGT  
25 661 TTAACCTTTTG GGCCATCCAT TCCTGGCTTT AATTTTACTG GTACAGTCTC AATAGGGCTA  
721 ATGGGAAAAA TTAAAGTGCA ACCAATCTGA GTCAACAGAT TTCTTCCAAT TATGTTGACA  
781 GGTGAGATGC CTACTAATAC TGTACCTATA GCTTTATGTC CACAGATTTC TATGAGTATC  
841 TGATCATACT GTCTTACTTT GATAAAACCT CCAATTCGCC CTATCATTTT TGGTTTCCAT  
901 CTTCTGGGCA AAGTCATTTC TTCTAATACT GTATCATCTG CTCTGTATC TAATAGAGCT  
30 961 TCCTTTAGTT GCCCCTCTAT CTTTATTGTG ACGAGGGGTC GTTGCCAAAG AGTGATCTGA  
1021 GGAAGTTTAA AGGATACAGT SEQ ID NO:37

Parent Sequence Accession No.: X01677

Locus: G3PDH (Clontech G3PDH template - parses into probes specific for antisense-strand target)

Length: 999

35 1 GAAGGTCGGA GTCAACGGAT TTGGTCGTAT TGGGCGCCTG GTCACCAGGG CTGCTTTTAA  
40 61 CTCTGGTAAA GTGCTATATTG TTGCCATCAA TGACCCCTTC ATTGACCTCA ACTACATGGT  
121 TTACATGTTT CATATGATT CCACCCATGG CAAATTCAT GGCACCGTCA AGGCTGAGAA  
181 CGGGAAGCTT GTCACTCAATG GAAATCCCAT CACCATCTTC CAGGAGCGAG ATCCCTCCAA  
241 AATCAAGTGG GCGCATGCTG GCGCTGAGTA CGTCTGGGAG TCCACTGGCG TCTTCAACCA  
301 CTTGGAGAAG GCTGGGGCTC ATTTGCAAGG GGGAGCCAAA AGGGTCTATCA TCTCTGCCCC  
45 361 CTCTGCTGAT GCCCCCATGT TCGTCATGGG TGTGAACCAT GAGAAGTATG ACAACAGCCT  
421 CAGATCATCT AGCAATGCCCT CCGTGCACCA CAACCTGCTTA GCACCCCTGG CCAAGGTGAT  
481 CCATGACACR TTTGGTATCG TGGAAGGACT CTGATGCCCA CTGATGCCCA TCACTGGCAC  
541 CCAGAAAGACT GTGGATGGCC CCTCCGGGAA ACTGTGGCGT GATGGGCGCG GGGCTCTCCA  
601 GAACATCATC CTGCTCTCTA CTGGCGCTGC CAAGGCTGTG GGCAAGGTCA TCCTGAGCT  
50 661 AGACGGGAAG CTCACTGGCA TGGCCTTCGG TGTCCCATCT GCCAACGTGT CAGTGGTGGG  
721 CTCTGACCTGC CGTCTAGAAA AACCTGCCAA ATATGATGAC ATCAAGAAGG TGGTGAAGCA  
781 GGCCTCGGAG GGCCCTCTCA AAGGCATCCT GGGCTACACT GAGCACCAGG TTGTCTCTC  
841 TGACTTTCAAC AGCGACACC ACTCCTCCAC CTTTGAGCGT GGGCTGGCA TGGCTCTCAA  
901 CGACCACTTT GTCAAGCTCA TTTCTGGTA TGACACGAA TTTGGGTACA GCAACAGGGT  
55 961 GGTGGACCTC ATGGCCACCA TGCTATAGTG AGTCGTATT SEQ ID NO:38

Parent Sequence Accession No.: X54156

Locus: HSP53PCRa (p53 template - parses into probes specific for antisense-strand target)

Length: 1049

1 GAGGTGCGTG TTTGTGCCTG TCCTGGGAGA GACCGGCGCA CAGAGGAAGA GAATCTCCGC  
61 AAGAAAAGGG AGCCTCACCA CGAGCTGCC CCAGGGAGCA CTAAGCGAGC ACTGCCCAAC  
121 AACACCAGCT CCTCTCCCA GCCAAAGAAG AAACCACTGG ATGGAGAATA TTTCACCCCTT  
181 CAGATCCGTG GCGGTGAGCG CTTCCGAGATG TTCCGAGAGC TGAATGAGGC CTTGGAATCTC  
241 AAGGATGCCC AGGTGTTGGAA GGAGCCAGGG GGGAGCAGGG CTCACCTCCAG CCACCTGAAG  
301 TCCAAAAAGG GTCAGTCTAC CTCCCGCCAT AAAAACTCA TGTTCAGAGC AGAAGGGCCT  
361 GACTCAGACT GACATTCTCC ACTTCTTGTT CCCCACTGAC AGGCTCCCTC CCCCATCTCT  
421 CCCTCCCTGT CCATTTTGGG TTTTGGGTCT TTGAACCCCT GCTTGAATA GGTGTGCGTC  
481 AGAAGCACCC AGGACTTCCA TTTGCTTTGT CCCGGGGCTC CACTGAACAA GTTGGCCTGC  
541 ACTGGTGTIT TGTGTGGGG AGGAGGATGG GGAGTAGGAC ATACCAGCTT AGATTTTAAG  
601 GTTTTTACTG TGAGGGATGT TTGGGAGATG TAAGAAATGT TCTTGCAGTT AAGGGTTAGT  
661 TTCAAATCAG CCACATTCTA GGTAGGTAGG GGCCCACTTC ACCGTACTAA CCAGGGAAGC  
721 TGTCCCTCAT GTTGAATTTT CTCTAACTTC AAGGCCATA TCTGTGAAT GCTGGCATTT  
781 GCACCTACCT CACAGAGTGC ATTGTGAGGG TTAATGAAT AATGTACATC TGGCCTTGAA  
841 ACCACCTTTT ATTACATGGG GTCTAAACT TGACCCCTT GAGGGTGCTC GTTCCCTCTC  
901 CCTCTCCCTG TTGGCTGGTG GGTGTGGTAGT TTCTACAGTT GGGCAGCTGG TTAGGTAGAG  
961 GGAGTTGTCA AGTCTTGCTG GCCCAGCAA ACCCTGTCTG ACAACCTCTT GGTGACCTTT  
1021 AGTACCTAAA AGGAAATCTC ACCCCATCC SEQ ID NO:39

The sequences indicated above, which are complements of the target sequences, were divided into overlapping oligonucleotide sequences with one nucleotide between starting positions. The oligonucleotide sequence lengths were 17 (rabbit  $\beta$ -globin), 20 (HIV PRT) or 25 (G3PDH; p53). The oligonucleotide sequence lengths were dictated by the probe lengths used in the experiments to which the predictions were compared. The RNA target concentrations used to calculate predicted RNA/DNA duplex melting temperatures were 100 pM (rabbit  $\beta$ -globin), 26.3 nM (HIV PRT) and 10 nM (G3PDH; p53). These were also dictated by experimental conditions for the comparison data. The cut-off filter used for the predicted free energy of the most stable probe sequence intramolecular structure,

$\Delta G_{MFOLD}$ , was

$$\Delta G_{MFOLD} \geq -0.4 \frac{\text{kcal}}{\text{mole}}$$

The filter condition used for the predicted RNA/DNA duplex melting temperature was

$$25^{\circ}\text{C} \leq T_m + 16.6 \log([Na^+]) - T_{hyp} \leq 50^{\circ}\text{C}$$

where  $T_m$  is the target concentration-dependent value of the predicted RNA/DNA duplex melting temperature before correction for salt concentration, the term " $16.6 \log([Na^+])$ " corrects the melting temperature for salt effects, and  $T_{hyb}$  is the hybridization temperature. The values of the salt correction term and  $T_{hyb}$  have already been listed in Table 2. For convenient use within p5, the above condition was algebraically rearranged into the equivalent form

$$25^{\circ}C - 16.6 \log([Na^+]) + T_{hyb} \leq T_m \leq 50^{\circ}C - 16.6 \log([Na^+]) + T_{hyb}.$$

Clusters were ranked according to the number of contiguous oligonucleotide sequences that passed through the filter set ("contig" length).

Results: The detailed analysis results for rabbit  $\beta$ -globin are presented in Table 3; a graphical summary of the results is shown in Fig. 4. In Table 3, values of  $T_m$  and  $\Delta G_{MFOLD}$  that were excluded by the filter set are shown with a line through them, and table entries for contig length are shown in gray when the oligonucleotide sequence in question was not in a contig. The top 20% of the observed hybridization intensities are shown underlined.

Table 3

| Position | Oligonucleotide Sequence | SEQ ID NO: | T <sub>m</sub> (°C) | ΔG <sub>Mfold</sub> (kcal/mole) | Contig Length | Hybridization Intensity (Milner <i>et al.</i> , 1997) |
|----------|--------------------------|------------|---------------------|---------------------------------|---------------|---|
| 1        | TTCTTCCACATTACCT         | 40         | <del>53.62</del>    | 5.00                            |               | 100   |
| 2        | TCTTCCACATTACCTT         | 41         | <del>53.62</del>    | 5.00                            |               | 130   |
| 3        | CTTCCACATTACCTTG         | 42         | <del>52.19</del>    | 0.90                            |               | 130   |
| 4        | TTCCACATTACCTTGC         | 43         | <del>54.60</del>    | 0.50                            |               | 200   |
| 5        | TCCACATTACCTTGCC         | 44         | 58.46               | 0.50                            | 7             | 120   |
| 6        | CCACATTACCTTGCCC         | 45         | 61.10               | 0.50                            | 7             | 180   |
| 7        | CACATTACCTTGCCCC         | 46         | 61.10               | 0.50                            | 7             | 230   |
| 8        | ACATTACCTTGCCCCA         | 47         | 61.10               | 0.50                            | 7             | 220   |
| 9        | CATTACCTTGCCCCAC         | 48         | 61.10               | 0.90                            | 7             | 320   |
| 10       | ATTACCTTGCCCCACA         | 49         | 61.10               | 0.70                            | 7             | 310   |
| 11       | TTCACCTTGCCCCACAG        | 50         | 61.33               | 0.50                            | 7             | 320   |
| 12       | TCACTTGCCCCACAGG         | 51         | 63.70               | <del>-0.60</del>                |               | 390   |
| 13       | CACCTTGCCCCACAGGG        | 52         | 64.85               | <del>-1.60</del>                |               | 410   |
| 14       | ACCTTGCCCCACAGGGC        | 53         | 68.01               | <del>-4.40</del>                |               | 240   |
| 15       | CCTTGCCCCACAGGGCA        | 54         | 68.63               | <del>-5.40</del>                |               | 50  |
| 16       | CTTGCCCCACAGGGCAG        | 55         | 64.95               | <del>-5.60</del>                |               | 20  |
| 17       | TTGCCCCACAGGGCAGT        | 56         | 66.31               | <del>-5.60</del>                |               | 20  |
| 18       | TGCCCCACAGGGCAGTG        | 57         | 65.79               | <del>-5.40</del>                |               | 20  |
| 19       | GCCCCACAGGGCAGTGA        | 58         | 67.37               | <del>-4.40</del>                |               | 20  |
| 20       | CCCCACAGGGCAGTGAC        | 59         | 63.42               | <del>-1.60</del>                |               | 40  |
| 21       | CCCACAGGGCAGTGACC        | 60         | 63.42               | <del>-1.40</del>                |               | 20  |
| 22       | CCACAGGGCAGTGACCG        | 61         | 59.85               | <del>-1.40</del>                |               | 20  |
| 23       | CACAGGGCAGTGACCGC        | 62         | 60.14               | <del>-1.00</del>                |               | 20  |
| 24       | ACAGGGCAGTGACCGCA        | 63         | 60.14               | <del>-0.50</del>                |               | 20  |
| 25       | CAGGGCAGTGACCGCAG        | 64         | 59.76               | <del>-0.50</del>                |               | 30  |
| 26       | AGGGCAGTGACCGCAGA        | 65         | 59.83               | <del>-0.50</del>                |               | 20  |
| 27       | GGGCAGTGACCGCAGAC        | 66         | 60.22               | <del>-0.50</del>                |               | 30  |
| 28       | GGCAGTGACCGCAGACT        | 67         | 59.53               | <del>-0.50</del>                |               | 30  |
| 29       | GCACTGACCGCAGACTT        | 68         | 57.06               | <del>-0.40</del>                |               | 30  |
| 30       | CAGTGACCGCAGACTTC        | 69         | <del>53.99</del>    | <del>-0.40</del>                |               | 40  |
| 31       | AGTGACCGCAGACTTCT        | 70         | <del>54.74</del>    | -0.20                           |               | 40  |
| 32       | GTGACCGCAGACTTCTC        | 71         | 55.99               | 0.60                            | 7             | 100   |
| 33       | TGACCGCAGACTTCTCC        | 72         | 57.01               | 0.60                            | 7             | 120   |
| 34       | GACCGCAGACTTCTCCT        | 73         | 59.22               | 0.60                            | 7             | 180   |
| 35       | ACCGCAGACTTCTCCTC        | 74         | 59.28               | 0.60                            | 7             | 210   |
| 36       | CCGCAGACTTCTCCTCA        | 75         | 60.07               | 0.60                            | 7             | 200   |
| 37       | CGCAGACTTCTCCTCAC        | 76         | 56.34               | 0.60                            | 7             | 190   |
| 38       | GCAGACTTCTCCTCACT        | 77         | 57.79               | 0.60                            | 7             | 240   |
| 39       | CAGACTTCTCCTCACTG        | 78         | <del>52.93</del>    | 0.60                            |               | 240   |
| 40       | AGACTTCTCCTCACTGG        | 79         | <del>54.44</del>    | 0.00                            |               | 340   |

Table 3

| Position | Oligonucleotide Sequence | SEQ ID NO. | T <sub>m</sub> (°C) | ΔG <sub>Mfold</sub> (kcal/mole) | Contig Length | Hybridization Intensity (Milner <i>et al.</i> , 1997) |
|----------|--------------------------|------------|---------------------|---------------------------------|---------------|---|
| 41       | GACTTCTCTCACTGGA         | 80         | 55.77               | -1.40                           |               | 340   |
| 42       | ACTTCTCTCACTGGAC         | 81         | 54.85               | -1.60                           |               | 240   |
| 43       | CTTCTCTCTCACTGGACA       | 82         | 55.75               | -1.60                           |               | 240   |
| 44       | TCTCTCTCACTGGACAG        | 83         | 53.66               | -1.60                           |               | 120   |
| 45       | TCTCTCACTGGACAGA         | 84         | 54.82               | -1.60                           |               | 100   |
| 46       | CTCTCACTGGACAGAT         | 85         | 53.36               | -1.60                           |               | 110   |
| 47       | TCCTCACTGGACAGATG        | 86         | 54.10               | -1.40                           |               | 80  |
| 48       | CCTCACTGGACAGATGC        | 87         | 54.25               | 0.00                            |               | 240   |
| 49       | CTCACTGGACAGATGCA        | 88         | 54.26               | 0.20                            |               | 90  |
| 50       | TCACTGGACAGATGCAC        | 89         | 49.63               | 0.20                            |               | 30  |
| 51       | CACTGGACAGATGCACC        | 90         | 52.74               | 0.50                            |               | 100   |
| 52       | ACTGGACAGATGCACCA        | 91         | 52.74               | -0.50                           |               | 80  |
| 53       | CTGGACAGATGCACCAT        | 92         | 52.18               | -1.00                           |               | 90  |
| 54       | TGGACAGATGCACCAT         | 93         | 50.39               | -0.80                           |               | 80  |
| 55       | GGACAGATGCACCATTC        | 94         | 54.75               | 0.30                            |               | 180   |
| 56       | GACAGATGCACCATCT         | 95         | 54.05               | -0.10                           |               | 220   |
| 57       | ACAGATGCACCATCTG         | 96         | 49.56               | -1.80                           |               | 120   |
| 58       | CAGATGCACCATCTGT         | 97         | 52.19               | -2.40                           |               | 120   |
| 59       | AGATGCACCATCTGTCT        | 98         | 52.06               | -0.10                           |               | 250   |
| 60       | GATGCACCATCTGTCT         | 99         | 54.18               | 0.30                            |               | 520   |
| 61       | ATGCACCATCTGTCTGT        | 100        | 52.60               | 0.40                            |               | 980   |
| 62       | TGCACCATCTGTCTGT         | 101        | 56.05               | 0.20                            | 2             | 780   |
| 63       | GCACCATCTGTCTGTT         | 102        | 56.52               | 0.20                            | 2             | 810   |
| 64       | CACCATCTGTCTGTTT         | 103        | 52.06               | 0.20                            |               | 220   |
| 65       | ACCATCTGTCTGTTTT         | 104        | 50.83               | 0.20                            |               | 120   |
| 66       | CCATTCTGTCTGTTTTG        | 105        | 50.18               | 0.20                            |               | 120   |
| 67       | CATTCTGTCTGTTTTGG        | 106        | 48.42               | 0.60                            |               | 160   |
| 68       | ATTCTGTCTGTTTTGGG        | 107        | 49.94               | 1.70                            |               | 310   |
| 69       | TTCTGTCTGTTTTGGGG        | 108        | 53.40               | 1.70                            |               | 250   |
| 70       | TCTGTCTGTTTTGGGGG        | 109        | 55.90               | 1.70                            | 2             | 80  |
| 71       | CTGTCTGTTTTGGGGGA        | 110        | 55.91               | 1.40                            | 2             | 30  |
| 72       | TGTCTGTTTTGGGGGAT        | 111        | 53.55               | 0.90                            |               | 50  |
| 73       | GTCGTGTTTTGGGGGATT       | 112        | 54.00               | 0.90                            |               | 10  |
| 74       | TCTGTTTTGGGGGATTG        | 113        | 50.50               | 1.10                            |               | 10  |
| 75       | CTGTTTTGGGGGATTGC        | 114        | 53.77               | 2.20                            |               | 10  |
| 76       | TGTTTTGGGGGATTGCA        | 115        | 53.04               | 1.20                            |               | 10  |
| 77       | GTTTTGGGGGATTGCAA        | 116        | 54.04               | 0.00                            |               | 5   |
| 78       | TTTTGGGGGATTGCAAG        | 117        | 47.00               | -0.20                           |               | 5   |
| 79       | TTTGGGGGATTGCAAGT        | 118        | 50.80               | -0.20                           |               | 5   |
| 80       | TTGGGGGATTGCAAGTA        | 119        | 49.80               | 0.00                            |               | 5   |

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Table 3

| Position | Oligonucleotide Sequence | SEQ ID NO: | T <sub>m</sub> (°C) | ΔG <sub>Mfold</sub> (kcal/mole) | Contig Length | Hybridization Intensity (Milner <i>et al.</i> , 1997) |
|----------|--------------------------|------------|---------------------|---------------------------------|---------------|---|
| 81       | TGGGGGATTGCAAGTAA        | 120        | 47.55               | 1.20                            |               | 5   |
| 82       | GGGGGATTGCAAGTAAA        | 121        | 45.76               | 1.40                            |               | 5   |
| 83       | GGGGATTGCAAGTAAAC        | 122        | 43.54               | 1.40                            |               | 5   |
| 84       | GGGATTGCAAGTAAACA        | 123        | 42.32               | 1.30                            |               | 5   |
| 85       | GGATTGCAAGTAAACAC        | 124        | 40.44               | 0.90                            |               | 5   |
| 86       | GATTGCAAGTAAACACA        | 125        | 38.94               | 0.50                            |               | 5   |
| 87       | ATTGCAAGTAAACACAG        | 126        | 37.64               | 0.50                            |               | 5   |
| 88       | TTGCAAGTAAACACAGT        | 127        | 40.35               | 0.50                            |               | 5   |
| 89       | TGCAAGTAAACACAGTT        | 128        | 40.35               | 0.30                            |               | 5   |
| 90       | GCAAGTAAACACAGTTG        | 129        | 40.35               | 0.10                            |               | 10  |
| 91       | CAAGTAAACACAGTTGT        | 130        | 38.98               | -0.30                           |               | 5   |
| 92       | AAGTAAACACAGTTGTG        | 131        | 37.40               | -0.90                           |               | 5   |
| 93       | AGTAAACACAGTTGTGT        | 132        | 42.02               | -2.30                           |               | 5   |
| 94       | GTAACACAGTTGTGTC         | 133        | 43.15               | -2.50                           |               | 5   |
| 95       | TAAACACAGTTGTGTCA        | 134        | 44.73               | -2.50                           |               | 5   |
| 96       | AAACACAGTTGTGTCAA        | 135        | 40.67               | -2.50                           |               | 5   |
| 97       | AACACAGTTGTGTCAAA        | 136        | 40.67               | -2.50                           |               | 5   |
| 98       | ACACAGTTGTGTCAAAA        | 137        | 40.67               | -2.30                           |               | 10  |
| 99       | CACAGTTGTGTCAAAAG        | 138        | 40.20               | -4.20                           |               | 15  |
| 100      | ACAGTTGTGTCAAAAGC        | 139        | 42.93               | -0.50                           |               | 30  |
| 101      | CAGTTGTGTCAAAAGCA        | 140        | 43.99               | 0.20                            |               | 25  |
| 102      | AGTTGTGTCAAAAGCAA        | 141        | 40.67               | -0.10                           |               | 25  |
| 103      | GTTGTGTCAAAAGCAAG        | 142        | 40.67               | -0.30                           |               | 20  |
| 104      | TTGTGTCAAAAGCAAGT        | 143        | 40.67               | -0.10                           |               | 120   |
| 105      | TGTGTCAAAAGCAAGTG        | 144        | 40.40               | 0.50                            |               | 20  |

In Fig. 4, the hybridization intensity observed experimentally is plotted as a function of oligonucleotide starting position in the target-complementary sequence that was input into p5. The identified contigs are plotted as horizontal bars, with the contig rank (by length) shown in parentheses next to each bar. It is clear from Table 3 and Fig. 4 that the prediction algorithm identified contigs that overlap all of the “top 20%” hybridization intensity peaks observed. Iterative experimental improvement of these predictions would converge on each of the observed intensity maxima in 3-4 iterations.

Prediction worksheets for HIV PRT, G3PDH and p53 were prepared in a manner similar to that for rabbit β-globin as shown in Table 3, except that the probes were longer as indicated above and that approximately 1,000 probes were

analyzed for each of these genes. The results of these analyses are shown in Fig. 5 (HIV PRT), Fig. 6 (G3PDH) and Fig. 7 (p53). In Fig. 5, data are plotted for all possible 20-mer oligonucleotide probes. In Figs. 6 and 7, data were available for only every 10<sup>th</sup> 25-mer probe, and the actual data points are plotted as open diamonds.

It is clear from Figs. 5-7 that the hybridization efficiency prediction algorithm of the present invention performed well in the task of identifying regions with observed high hybridization intensity. In each case, the 4 longest contigs point to good-to-excellent regions for experimental investigation. It should be noted that the contigs usually bracket observed intensity peaks; experimental iterative refinement would therefore be expected to converge in 2-3 iterations. By this is meant that certain oligonucleotides from the identified contigs are prepared and subjected to evaluation in actual hybridization experiments. Based on the results of such experiments, the observed signal is evaluated to determine whether the oligonucleotides are hybridizing to the left of, the right of, or on the center of a peak with respect to the graphed data. The next iteration is carried out to experimentally evaluate the hybridization efficiency of probes that are inferred to lie closer to the peak of hybridization efficiency, based on the data from the previous iteration. Iteration is continued until the signal level is deemed acceptable by the user, or the local hybridization efficiency maximum is reached (i.e. the best probe in the cluster identified by the method of the current invention has been experimentally identified). A detailed illustration of this process is shown in Example 3.

It should be noted that clusters of predictions that overlap the maxima of observed peaks of hybridization efficiency will often yield user-acceptable probes on the first iteration. Thus, the method of the present invention is much more efficient than current methods in which every potential probe is synthesized. For instance, in the HIV PRT example shown in Fig. 5, at least 3 good probes would be identified after synthesis of ~10 test probes (i.e. statistical sampling of the 3 longest contigs). This is much more efficient than the ~1,000 probes represented by the data in Fig. 5.

Example 2

Synopsis: Data from a labeled RNA target hybridization to an Affymetrix GeneChip™ HIV PRT-sense probe array (GeneChip™ HIV PRT 440s, Affymetrix Corporation, Santa Clara, CA) were compared to the predictions of the window-averaged composite dimensionless score version of the method of the present invention.

Materials and Methods: Data were obtained as described for the Affymetrix GeneChip™ HIV PRT-sense probe array (GeneChip™ HIV PRT 440s, Affymetrix Corporation, Santa Clara, California) in Example 1. The DNA sequence (SEQ ID NO: 37) complementary to the fluorescein-labeled RNA target was divided into overlapping 20-mer oligonucleotide sequences spaced one nucleotide apart, using the prototype application p5; p5 was also used to calculate the predicted values of the RNA/DNA heteroduplex melting temperature ( $T_m$ ) and the free energy of the most stable predicted probe intramolecular structure,  $\Delta G_{MFOLD}$ , as described in Example 1. The probe sequences and parameter values were then transferred to a Microsoft Excel spreadsheet, which was used to complete the predictions of efficient and inefficient probes. The weight was obtained by optimizing the performance of the algorithm with the data of Milner *et al.*, *supra*, as the training data using the Microsoft® Excel® spreadsheet software. The composite score was calculated using a weight of 0.62 for the dimensionless  $T_m$  score and a weight of 0.38 for the  $\Delta G_{MFOLD}$  dimensionless score. The windowed-averaging was performed using a window width of 7 and Microsoft® Excel® spreadsheet software. Finally, the oligonucleotide sequences having the top 10% of the window-averaged composite dimensionless scores were predicted to be efficient probes, while the oligonucleotide sequences having the bottom 10% of the window-averaged composite dimensionless scores were predicted to be inefficient probes.

Results: The calculated parameters and scores are shown in Table 4; the algorithm predictions are also shown diagrammatically in Figure 8. In Table 4, window-averaged composite score values that were in the top 10% of the

distribution of values are shown in bold type, values that were in the bottom 10% are shown in italics, and all other values are shown with a line through them. It is clear from both Table 4 and Figure 8 that the window-averaged composite dimensionless score embodiment of the current invention correctly predicted both efficient and inefficient hybridization probes for HIV PRT sense-strand RNA. As in Example 1, statistical sampling of contiguous stretches of predicted "good" probes would lead to convergence of the design process to the best probes in each region in 2-4 design iterations.

Table 4

| p5 Probe Position | DNA Probe Sequence    | SEQ ID NO: | RNA/DNA T <sub>m</sub> (°C) | $\Delta G_{\text{fold}}$ (kcal/mole @ 35 °C) | T <sub>m</sub> Score | $\Delta G_{\text{fold}}$ Score | Composite Score | Window-Averaged Composite Score | HIV PRT GeneChip™ Data |
|-------------------|-----------------------|------------|-----------------------------|--|----------------------|--------------------------------|-----------------|---------------------------------|------------------------|
| 1                 | GTACTGTCCTATTATCAGGA  | 145        | 64.16                       | -0.10  | 0.557                | -0.199                         | 0.269           |                                 | 1152.2                 |
| 2                 | TACTGTCCTATTATCAGGAT  | 146        | 60.91                       | -0.40  | 0.080                | -0.460                         | -0.125          |                                 | 1040.7                 |
| 3                 | ACTGTCCTATTATCAGGATG  | 147        | 61.41                       | -0.90  | 0.152                | -0.895                         | -0.246          |                                 | 291.9                  |
| 4                 | CTGTCCTATTATCAGGATGG  | 148        | 63.46                       | -0.90  | 0.453                | -0.895                         | -0.069          | -0.168                          | 221.8                  |
| 5                 | GTGTCCTATTATCAGGATGGA | 149        | 62.82                       | -0.90  | 0.360                | -0.895                         | -0.117          | -0.284                          | 148.3                  |
| 6                 | GTCCTATTATCAGGATGGAG  | 150        | 63.15                       | -1.90  | 0.408                | -1.764                         | -0.418          | -0.308                          | 84.6                   |
| 7                 | TCCATTATCAGGATGGAGT   | 151        | 63.15                       | -2.10  | 0.408                | -1.938                         | -0.484          | -0.262                          | 128.7                  |
| 8                 | CNNTTATCAGGATGGAGTT   | 152        | 62.03                       | -1.90  | 0.245                | -1.764                         | -0.519          | -0.242                          | 94.6                   |
| 9                 | CATTATCAGGATGGAGTTTC  | 153        | 59.53                       | -0.80  | -0.122               | -0.634                         | -0.317          | -0.236                          | 157.5                  |
| 10                | ATTATCAGGATGGAGTTCA   | 154        | 59.53                       | 0.80   | -0.122               | 0.583                          | 0.146           | -0.227                          | 316.9                  |
| 11                | TTTATCAGGATGGAGTTCA   | 155        | 59.53                       | 0.40   | -0.122               | 0.236                          | 0.014           | -0.194                          | 360.2                  |
| 12                | TTATCAGGATGGAGTTCA    | 156        | 58.58                       | 0.40   | -0.262               | 0.236                          | -0.073          | -0.106                          | 403.8                  |
| 13                | TATCAGGATGGAGTTCA     | 157        | 56.21                       | 0.20   | -0.609               | 0.062                          | -0.354          | -0.044                          | 382.5                  |
| 14                | ATCAGGATGGAGTTCA      | 158        | 57.34                       | 0.20   | -0.444               | 0.062                          | -0.252          | -0.004                          | 324.4                  |
| 15                | TCAGGATGGAGTTCA       | 159        | 61.25                       | 0.20   | 0.129                | 0.062                          | 0.104           | -0.036                          | 320.5                  |
| 16                | CAGGATGGAGTTCA        | 160        | 63.57                       | 0.20   | 0.470                | 0.062                          | 0.315           | -0.104                          | 238.9                  |
| 17                | AGGATGGAGTTCA         | 161        | 63.57                       | -0.10  | 0.470                | -0.199                         | 0.216           | -0.162                          | 202.3                  |
| 18                | GATGGAGTTCA           | 162        | 63.34                       | -1.30  | 0.436                | -1.243                         | -0.202          | -0.190                          | 113.6                  |
| 19                | GATGGAGTTCA           | 163        | 62.24                       | -2.00  | 0.275                | -1.851                         | -0.533          | -0.099                          | 97.7                   |
| 20                | ATGGAGTTCA            | 164        | 64.62                       | -3.30  | 0.624                | -2.982                         | -0.746          | -0.100                          | 143.3                  |
| 21                | TGGAGTTCA             | 165        | 68.18                       | -2.00  | 1.146                | -1.851                         | 0.007           | -0.109                          | 484.6                  |
| 22                | GGAGTTCA              | 166        | 69.39                       | -1.60  | 1.324                | -1.504                         | 0.249           | -0.068                          | 857.6                  |
| 23                | GAGTTCA               | 167        | 64.93                       | -0.20  | 0.670                | -0.286                         | 0.307           | 0.053                           | 991.4                  |
| 24                | AGTTCA                | 168        | 61.82                       | 0.20   | 0.213                | 0.062                          | 0.155           | 0.173                           | 907.0                  |
| 25                | GTTCA                 | 169        | 61.82                       | 0.20   | 0.213                | 0.062                          | 0.155           | 0.137                           | 887.9                  |
| 26                | TTCA                  | 170        | 61.36                       | 0.80   | 0.145                | 0.410                          | 0.246           | 0.053                           | 1015.3                 |

Table 4

| p5 Probe Position | DNA Probe Sequence    | SEQ ID NO: | RNA/DNA $T_m$ (°C) | $\Delta G_{fold}$ (kcal/mole @ 35 °C) | $T_m$ Score | $\Delta G_{fold}$ Score | Composite Score | Window-Averaged Composite Score | HIV PRT GeneChip™ Data |
|-------------------|-----------------------|------------|--------------------|---------------------------------------|-------------|-------------------------|-----------------|---------------------------------|------------------------|
| 27                | TCATACCACTCCCAAGGA    | 171        | 62.21              | -0.10                                 | 0.270       | -0.199                  | 0.092           | -0.049                          | 279.7                  |
| 28                | CATACCACTCCCAAGGAA    | 172        | 59.26              | -0.30                                 | -0.163      | -0.373                  | -0.243          | -0.124                          | 210.7                  |
| 29                | ATAACCACTCCCAAGGAAT   | 173        | 58.19              | -0.30                                 | -0.320      | -0.373                  | -0.340          | -0.204                          | 179.9                  |
| 30                | TAAACCACTCCCAAGGAATG  | 174        | 58.13              | -0.30                                 | -0.328      | -0.373                  | -0.345          | -0.309                          | 91.8                   |
| 31                | AACCACTCCCAAGGAATGG   | 175        | 60.78              | -1.30                                 | 0.061       | -1.243                  | -0.435          | -0.412                          | 44.6                   |
| 32                | ACCACTCCCAAGGAATGGA   | 176        | 63.69              | -2.00                                 | 0.487       | -1.851                  | -0.401          | -0.488                          | 42.9                   |
| 33                | CCAACCTCCCAAGGAATGGAG | 177        | 63.40              | -2.20                                 | 0.445       | -2.025                  | -0.494          | -0.542                          | 45.0                   |
| 34                | CAACCTCCCAAGGAATGGAGG | 178        | 62.34              | -2.30                                 | 0.290       | -2.112                  | -0.623          | -0.570                          | 45.3                   |
| 35                | CATCCCAAGGAATGGAGGT   | 179        | 61.72              | -2.60                                 | 0.199       | -2.373                  | -0.778          | -0.587                          | 47.9                   |
| 36                | ATCCCAAGGAATGGAGTT    | 180        | 60.90              | -2.20                                 | 0.079       | -2.025                  | -0.721          | -0.580                          | 49.2                   |
| 37                | TCCCAAGGAATGGAGTTCT   | 181        | 62.24              | -2.20                                 | 0.274       | -2.025                  | -0.600          | -0.585                          | 74.2                   |
| 38                | CCCAAGGAATGGAGTTCTT   | 182        | 62.71              | -2.00                                 | 0.344       | -1.851                  | -0.490          | -0.572                          | 125.5                  |
| 39                | CCAAGGAATGGAGTTCTT    | 183        | 59.47              | -0.70                                 | -0.132      | -0.721                  | -0.356          | -0.485                          | 183.3                  |
| 40                | CAAGGAATGGAGTTCTTT    | 184        | 56.10              | -0.30                                 | -0.627      | -0.373                  | -0.530          | -0.380                          | 261.4                  |
| 41                | AAGGAATGGAGTTCTTCT    | 185        | 56.11              | -0.30                                 | -0.625      | -0.373                  | -0.529          | -0.277                          | 518.3                  |
| 42                | AGGAATGGAGTTCTTCTT    | 186        | 60.05              | -0.30                                 | -0.046      | -0.373                  | -0.170          | -0.206                          | 716.5                  |
| 43                | AGGAATGGAGTTCTTCTG    | 187        | 62.09              | -0.30                                 | 0.253       | -0.373                  | 0.015           | -0.164                          | 1086.0                 |
| 44                | GAATGGAGTTCTTCTGGA    | 188        | 63.23              | -0.30                                 | 0.420       | -0.373                  | 0.119           | -0.025                          | 1084.3                 |
| 45                | GATGGAGTTCTTCTGAT     | 189        | 60.56              | 0.10                                  | 0.028       | -0.025                  | 0.008           | 0.119                           | 1241.1                 |
| 46                | ATGGAGTTCTTCTGATG     | 190        | 59.12              | 0.30                                  | -0.183      | 0.149                   | -0.057          | 0.212                           | 1278.8                 |
| 47                | TGGAGTTCTTCTGATGT     | 191        | 64.58              | 0.30                                  | 0.618       | 0.149                   | 0.440           | 0.268                           | 1616.0                 |
| 48                | AGGAGTTCTTCTGATGTT    | 192        | 64.98              | 0.30                                  | 0.677       | 0.149                   | 0.476           | 0.270                           | 1677.5                 |
| 49                | GAGGTTCTTCTGATGTTT    | 193        | 65.49              | 0.30                                  | 0.751       | 0.149                   | 0.522           | 0.300                           | 1963.1                 |
| 50                | GAGTTCTTCTGATGTTTT    | 194        | 63.04              | 0.30                                  | 0.392       | 0.149                   | 0.300           | 0.301                           | 2126.1                 |
| 51                | AGTTCTTCTGATGTTTTT    | 195        | 61.97              | 0.30                                  | 0.235       | 0.149                   | 0.202           | 0.234                           | 2143.3                 |
| 52                | GGTTCTTCTGATGTTTTT    | 196        | 62.11              | 0.30                                  | 0.256       | 0.149                   | 0.215           | 0.180                           | 3540.6                 |
| 53                | GTCTTCTGATGTTTTTT     | 197        | 59.21              | 0.30                                  | -0.170      | 0.149                   | -0.049          | 0.164                           | 1728.7                 |

Table 4

| p5 Probe Position | DNA Probe Sequence      | SEQ ID NO: | RNA/DNA T <sub>m</sub> (°C) | $\Delta G_{fold}$ (kcal/mole @ 35 °C) | T <sub>m</sub> Score | $\Delta G_{fold}$ Score | Composite Score | Window-Averaged Composite Score | HIV PRT GeneChip™ Data |
|-------------------|-------------------------|------------|-----------------------------|---------------------------------------|----------------------|-------------------------|-----------------|---------------------------------|------------------------|
| 54                | TTCTTCTGATGTTTTTGT      | 198        | 59.21                       | 0.30                                  | -0.170               | 0.149                   | -0.049          | 0.154                           | 1364.3                 |
| 55                | CTTCTTGATGTTTTTGTG      | 199        | 60.35                       | 0.50                                  | -0.002               | 0.323                   | 0.121           | 0.183                           | 1788.4                 |
| 56                | CTTCTGATGTTTTTGTCT      | 200        | 60.96                       | 1.20                                  | 0.086                | 0.931                   | 0.407           | 0.353                           | 2670.9                 |
| 57                | TTCTGATGTTTTTGTCTG      | 201        | 58.76                       | 1.20                                  | -0.235               | 0.931                   | 0.208           | 0.338                           | 3336.2                 |
| 58                | TTCTGATGTTTTTGTCTGG     | 202        | 61.17                       | 1.20                                  | 0.118                | 0.931                   | 0.427           | 0.440                           | 6683.6                 |
| 59                | CTGATGTTTTTGTCTGCT      | 203        | 64.20                       | 1.20                                  | 0.562                | 0.931                   | 0.702           | 0.532                           | 10227.0                |
| 60                | CTGATGTTTTTGTCTGCTG     | 204        | 62.51                       | 1.20                                  | 0.315                | 0.931                   | 0.549           | 0.625                           | 10965.0                |
| 61                | TGATGTTTTTGTCTGCTG      | 205        | 63.80                       | 1.20                                  | 0.504                | 0.931                   | 0.666           | 0.728                           | 11133.0                |
| 62                | ATGTTTTTGTCTGCTGCTG     | 206        | 63.80                       | 1.60                                  | 0.504                | 1.279                   | 0.798           | 0.894                           | 11503.0                |
| 63                | ATGTTTTTGTCTGCTGCTG     | 207        | 65.18                       | 1.90                                  | 0.705                | 1.540                   | 1.023           | 0.894                           | 9492.8                 |
| 64                | TGTTTTTGTCTGCTGCTG      | 208        | 68.78                       | 1.70                                  | 1.234                | 1.366                   | 1.284           | 0.914                           | 10704.0                |
| 65                | GTTTTTTGTCTGCTGCTGA     | 209        | 68.28                       | 1.70                                  | 1.161                | 1.366                   | 1.239           | 0.933                           | 10741.0                |
| 66                | TTTTTGTCTGCTGCTGCTGA    | 210        | 62.37                       | 1.70                                  | 0.294                | 1.366                   | 0.701           | 0.950                           | 9187.5                 |
| 67                | TTTTTGTCTGCTGCTGCTAG    | 211        | 62.23                       | 1.70                                  | 0.273                | 1.366                   | 0.689           | 0.941                           | 7871.0                 |
| 68                | TTTGTCTGCTGCTGCTAGT     | 212        | 65.28                       | 1.20                                  | 0.721                | 0.931                   | 0.801           | 0.921                           | 7209.1                 |
| 69                | TTTGTCTGCTGCTGCTAGTC    | 213        | 66.56                       | 1.20                                  | 0.908                | 0.931                   | 0.917           | 0.959                           | 8052.3                 |
| 70                | TTTGTCTGCTGCTGCTAGTCC   | 214        | 70.25                       | 0.30                                  | 1.449                | 0.149                   | 0.955           | 1.022                           | 7230.6                 |
| 71                | TGCTGCTGCTGCTGCTAGTCCC  | 215        | 73.77                       | -0.10                                 | 1.966                | -0.199                  | 1.143           | 0.988                           | 6809.5                 |
| 72                | GTCTGCTGCTGCTGCTAGTCCC  | 216        | 77.74                       | -0.10                                 | 2.549                | -0.199                  | 1.504           | 0.913                           | 7442.8                 |
| 73                | CTGCTGCTGCTGCTGCTAGTCCC | 217        | 75.28                       | -0.50                                 | 2.187                | -0.938                  | 1.148           | 0.824                           | 2627.7                 |
| 74                | CTGCTGCTGCTGCTGCTAGTCCC | 218        | 74.18                       | -2.10                                 | 2.026                | -1.937                  | 0.519           | 0.784                           | 1315.0                 |
| 75                | TGCTGCTGCTGCTGCTAGTCCC  | 219        | 75.80                       | -3.50                                 | 2.263                | -3.156                  | 0.204           | 0.690                           | 4182.3                 |
| 76                | GGTGTGCTGCTGCTGCTAGTCCC | 220        | 77.89                       | -3.80                                 | 2.571                | -3.417                  | 0.296           | 0.648                           | 474.7                  |
| 77                | GTGCTGCTGCTGCTGCTAGTCCC | 221        | 77.05                       | -2.50                                 | 2.448                | -2.286                  | 0.649           | 0.429                           | 682.4                  |
| 78                | GTGCTGCTGCTGCTGCTAGTCCC | 222        | 74.71                       | -2.50                                 | 2.105                | -2.286                  | 0.436           | 0.465                           | 679.1                  |
| 79                | GTGCTGCTGCTGCTGCTAGTCCC | 223        | 72.54                       | -2.10                                 | 1.785                | -1.938                  | 0.370           | 0.584                           | 924.0                  |
| 80                | TGCTGCTGCTGCTGCTAGTCCC  | 224        | 69.94                       | -0.90                                 | 1.404                | -0.895                  | 0.531           | 0.667                           | 835.5                  |

Table 4

| p5 Probe Position | DNA Probe Sequence   | SEQ ID NO: | RNA/DNA T <sub>m</sub> (°C) | $\Delta G_{\text{fold}}$ (Kcal/mole @ 35 °C) | T <sub>m</sub> Score | $\Delta G_{\text{fold}}$ Score | Composite Score | Window-Averaged Composite Score | HIV PRT GeneChip™ Data |
|-------------------|----------------------|------------|-----------------------------|--|----------------------|--------------------------------|-----------------|---------------------------------|------------------------|
| 81                | GGTAAGTCCCACTCAACA   | 225        | 71.14                       | -0.50  | 1.580                | -0.547                         | 0.772           | 0.632                           | 1213.6                 |
| 82                | GTAAGTCCCACTCAACAG   | 226        | 68.97                       | 0.90   | 1.262                | 0.670                          | 1.037           | 0.263                           | 1106.1                 |
| 83                | TAAAGTCCCACTCAACAGA  | 227        | 67.18                       | 0.90   | 0.999                | 0.870                          | 0.874           | 0.872                           | 1009.0                 |
| 84                | AAGTCCCACTCAACAGAT   | 228        | 67.68                       | 0.50   | 1.073                | 0.323                          | 0.788           | 0.908                           | 1656.2                 |
| 85                | AGTCCCACTCAACAGATG   | 229        | 69.68                       | 0.50   | 1.366                | 0.323                          | 0.970           | 0.434                           | 2178.3                 |
| 86                | TCCCACTCAACAGATGT    | 230        | 72.56                       | 0.20   | 1.789                | 0.062                          | 1.132           | 0.674                           | 2567.0                 |
| 87                | CCCACTCAACAGATGTT    | 231        | 69.77                       | -0.10  | 1.379                | -0.199                         | 0.779           | 0.522                           | 3000.5                 |
| 88                | CCCACTCAACAGATGTG    | 232        | 68.19                       | -1.30  | 1.148                | -1.243                         | 0.240           | 0.364                           | 2025.4                 |
| 89                | CCCACTCAACAGATGTGC   | 233        | 67.78                       | -2.00  | 1.087                | -1.851                         | -0.030          | 0.464                           | 429.2                  |
| 90                | CCCACTCAACAGATGTGTC  | 234        | 65.65                       | -2.00  | 0.775                | -1.851                         | -0.223          | -0.041                          | 157.9                  |
| 91                | CACCTCAACAGATGTGTCT  | 235        | 63.85                       | -2.00  | 0.511                | -1.851                         | -0.387          | -0.244                          | 135.3                  |
| 92                | ACCTCAACAGATGTGTCTCA | 236        | 64.11                       | -2.00  | 0.549                | -1.851                         | -0.363          | -0.339                          | 330.8                  |
| 93                | CTCTCAACAGATGTGTCTCA | 237        | 64.77                       | -2.00  | 0.646                | -1.851                         | -0.303          | -0.370                          | 900.0                  |
| 94                | CTCAACAGATGTGTCTCAG  | 238        | 61.08                       | -2.00  | 0.104                | -1.851                         | -0.639          | -0.300                          | 1177.0                 |
| 95                | TCAACAGATGTGTCTCAGC  | 239        | 63.40                       | -2.00  | 0.444                | -1.851                         | -0.428          | -0.412                          | 795.1                  |
| 96                | CAACAGATGTGTCTCAGCT  | 240        | 63.91                       | -1.60  | 0.520                | -1.504                         | -0.249          | 0.081                           | 889.2                  |
| 97                | AACAGATGTGTCTCAGCTC  | 241        | 64.19                       | -0.10  | 0.560                | -0.199                         | 0.272           | 0.282                           | 1703.6                 |
| 98                | ACAGATGTGTCTCAGCTCC  | 242        | 70.61                       | 0.00   | 1.503                | -0.112                         | 0.889           | 0.508                           | 3115.2                 |
| 99                | CAGATGTGTCTCAGCTCTC  | 243        | 72.08                       | 0.00   | 1.719                | -0.112                         | 1.023           | 0.847                           | 4445.0                 |
| 100               | AGATGTGTCTCAGCTCTCC  | 244        | 72.86                       | 0.20   | 1.803                | 0.062                          | 1.141           | 1.070                           | 6762.8                 |
| 101               | GATGTGTCTCAGCTCTCTCT | 245        | 74.49                       | 0.90   | 2.071                | 0.670                          | 1.539           | 1.227                           | 8845.0                 |
| 102               | TGTGTGTCTCAGCTCTCTA  | 246        | 72.38                       | 0.80   | 1.763                | 0.583                          | 1.314           | 1.253                           | 9010.6                 |
| 103               | TGTGTCTCAGCTCTCTCAT  | 247        | 72.38                       | 0.80   | 1.763                | 0.583                          | 1.314           | 1.280                           | 19941.0                |
| 104               | GTGTGTCTCAGCTCTCTATT | 248        | 72.97                       | 0.80   | 1.849                | 0.583                          | 1.368           | 1.257                           | 12577.0                |
| 105               | TGTGTCTCAGCTCTCTATT  | 249        | 69.70                       | 0.80   | 1.369                | 0.583                          | 1.071           | 1.149                           | 7503.3                 |
| 106               | TGTCTCAGCTCTCTATT    | 250        | 69.70                       | 0.80   | 1.369                | 0.583                          | 1.071           | 1.098                           | 7033.8                 |
| 107               | GTCCTCAGCTCTCTATT    | 251        | 70.26                       | 0.80   | 1.451                | 0.583                          | 1.121           | 1.024                           | 8276.7                 |

Table 4

| p5 Probe Position | DNA Probe Sequence     | SEQ ID NO: | RNA/DNA T <sub>m</sub> (°C) | $\Delta G_{\text{fold}}$ (kcal/mole @ 35 °C) | T <sub>m</sub> Score | $\Delta G_{\text{fold}}$ Score | Composite Score | Window-Averaged Composite Score | HIV PRT GeneChip™ Data |
|-------------------|------------------------|------------|-----------------------------|--|----------------------|--------------------------------|-----------------|---------------------------------|------------------------|
| 108               | TCTCAGCTCTCTATTTTGG    | 252        | 66.57                       | 0.80   | 0.910                | 0.583                          | 0.786           | 0.942                           | 2899.0                 |
| 109               | CTCAGCTCTCTATTTTGGT    | 253        | 68.39                       | 0.80   | 1.177                | 0.583                          | 0.952           | 0.923                           | 2935.0                 |
| 110               | TCAGCTCTCTATTTTGGT     | 254        | 66.69                       | 0.80   | 0.927                | 0.583                          | 0.796           | 0.930                           | 1512.8                 |
| 111               | CAGCTCTCTATTTTGGTGC    | 255        | 66.69                       | 0.80   | 0.927                | 0.583                          | 0.796           | 0.872                           | 1708.8                 |
| 112               | AGCTCTCTATTTTGGTCT     | 256        | 67.52                       | 1.00   | 1.050                | 0.757                          | 0.939           | 0.833                           | 1977.3                 |
| 113               | CTCTCTATTTTGGTCTGA     | 257        | 66.63                       | 1.80   | 0.919                | 1.453                          | 1.122           | 0.809                           | 2114.8                 |
| 114               | CTCTCTATTTTGGTCTAT     | 258        | 62.13                       | 1.80   | 0.259                | 1.453                          | 0.713           | 0.566                           | 1527.3                 |
| 115               | TCTCTATTTTGGTCTATGC    | 259        | 59.97                       | 1.80   | -0.058               | 1.453                          | 0.516           | 0.695                           | 1536.8                 |
| 116               | CTCTATTTTGGTCTATGC     | 260        | 62.84                       | 1.80   | 0.363                | 1.453                          | 0.777           | 0.642                           | 1824.5                 |
| 117               | CTCTATTTTGGTCTATGCT    | 261        | 60.87                       | 1.50   | 0.074                | 1.192                          | 0.499           | 0.698                           | 1169.2                 |
| 118               | TCATTTTGGTCTATGCTG     | 262        | 58.71                       | 1.50   | -0.244               | 1.192                          | 0.302           | 0.649                           | 683.7                  |
| 119               | CTATTTTGGTCTATGCTGC    | 263        | 61.60                       | 1.50   | 0.181                | 1.192                          | 0.565           | 0.768                           | 1306.8                 |
| 120               | TATTTTGGTCTATGCTGCC    | 264        | 63.53                       | 1.50   | 0.464                | 1.192                          | 0.741           | 0.834                           | 2523.6                 |
| 121               | ATTTTGGTCTATGCTGCC     | 265        | 67.96                       | 1.50   | 1.113                | 1.192                          | 1.143           | 0.931                           | 6682.0                 |
| 122               | TTTGGTCTATGCTGCCCT     | 266        | 69.96                       | 1.50   | 1.407                | 1.192                          | 1.325           | 1.060                           | 9417.4                 |
| 123               | TTTGGTCTATGCTGCCCTA    | 267        | 69.01                       | 1.50   | 1.267                | 1.192                          | 1.239           | 1.151                           | 10339.0                |
| 124               | TTTGGTCTATGCTGCCCTAT   | 268        | 68.62                       | 1.50   | 1.210                | 1.192                          | 1.203           | 1.254                           | 10750.0                |
| 125               | TTTGGTCTATGCTGCCCTATT  | 269        | 68.62                       | 1.50   | 1.210                | 1.192                          | 1.203           | 1.282                           | 11180.0                |
| 126               | TGTTCTATGCTGCCCTATTT   | 270        | 68.62                       | 1.50   | 1.210                | 1.192                          | 1.203           | 1.271                           | 11080.0                |
| 127               | GTTCTATGCTGCCCTATTTTC  | 271        | 70.37                       | 1.80   | 1.468                | 1.453                          | 1.462           | 1.221                           | 16074.0                |
| 128               | TTCTATGCTGCCCTATTTCT   | 272        | 69.00                       | 1.80   | 1.266                | 1.453                          | 1.337           | 1.144                           | 9183.8                 |
| 129               | CTATGCTGCCCTATTTCTA    | 273        | 68.05                       | 1.80   | 1.127                | 1.453                          | 1.251           | 1.082                           | 8617.8                 |
| 130               | CTATGCTGCCCTATTTCTTAA  | 274        | 64.38                       | 1.70   | 0.589                | 1.366                          | 0.884           | 1.040                           | 7286.8                 |
| 131               | TATGCTGCCCTATTTCTTAAG  | 275        | 62.71                       | 1.50   | 0.344                | 1.192                          | 0.666           | 0.978                           | 3642.4                 |
| 132               | ATGCTGCCCTATTTCTTAAGT  | 276        | 66.39                       | 0.80   | 0.883                | 0.583                          | 0.769           | 0.883                           | 3795.7                 |
| 133               | TCGCTGCCCTATTTCTTAAGTC | 277        | 67.95                       | 0.80   | 1.112                | 0.583                          | 0.911           | 0.749                           | 3408.3                 |
| 134               | GCTGCCCTATTTCTTAAGTCA  | 278        | 69.25                       | 0.80   | 1.303                | 0.583                          | 1.030           | 0.644                           | 4017.4                 |

Table 4

| p5 Probe Position | DNA Probe Sequence                  | SEQ ID NO: | RNA/DNA T <sub>m</sub> (°C) | $\Delta G_{\text{fold}}$ (kcal/mole @ 35 °C) | T <sub>m</sub> Score | $\Delta G_{\text{fold}}$ Score | Composite Score | Window-Averaged Composite Score | HIV PRT GeneChip™ Data |
|-------------------|-------------------------------------|------------|-----------------------------|--|----------------------|--------------------------------|-----------------|---------------------------------|------------------------|
| 135               | CTGCCCTATTCTTAAGTCAG                | 279        | 65.26                       | 0.80   | 0.718                | 0.583                          | 0.667           | 0.536                           | 2197.2                 |
| 136               | TGCCCTATTCTTAAGTCAGA                | 280        | 64.63                       | -0.10  | 0.626                | -0.199                         | 0.312           | 0.412                           | 1125.0                 |
| 137               | GCCTATTCTTAAGTCAGAT                 | 281        | 64.73                       | -0.60  | 0.639                | -0.634                         | 0.156           | 0.244                           | 1306.3                 |
| 138               | CCCTATTCTTAAGTCAGATC                | 282        | 61.98                       | -0.60  | 0.236                | -0.634                         | -0.094          | 0.024                           | 1019.5                 |
| 139               | CCATTCTTAAGTCAGATCC                 | 283        | 61.98                       | -0.60  | 0.236                | -0.634                         | -0.094          | -0.129                          | 1852.3                 |
| 140               | CTATTCTTAAGTCAGATCCT                | 284        | 60.05                       | -0.60  | -0.046               | -0.634                         | -0.270          | -0.214                          | 3150.3                 |
| 141               | TATTCTTAAGTCAGATCCCTA               | 285        | 57.43                       | -0.60  | -0.430               | -0.634                         | -0.508          | -0.284                          | 2604.8                 |
| 142               | ATTCTTAAGTCAGATCCCTAC               | 286        | 58.59                       | -0.60  | -0.261               | -0.634                         | -0.402          | -0.346                          | 3886.1                 |
| 143               | TTCTTAAGTCAGATCCCTACA               | 287        | 59.91                       | -0.60  | -0.068               | -0.634                         | -0.283          | -0.285                          | 4500.7                 |
| 144               | TTCTTAAGTCAGATCCCTACAT              | 288        | 59.55                       | -0.60  | -0.120               | -0.634                         | -0.315          | -0.233                          | 4754.5                 |
| 145               | TCTTAAGTCAGATCCCTACATA              | 289        | 58.62                       | -0.40  | -0.257               | -0.460                         | -0.334          | -0.165                          | 3802.1                 |
| 146               | CTAAGTCAGATCCCTACATAC               | 290        | 57.80                       | 1.20   | -0.377               | 0.931                          | 0.120           | -0.111                          | 5069.4                 |
| 147               | TAAGTCAGATCCCTACATACA               | 291        | 57.13                       | 1.30   | -0.476               | 1.018                          | 0.092           | -0.059                          | 3965.2                 |
| 148               | AGTCAGATCCCTACATACAAA               | 292        | 55.78                       | 1.30   | -0.673               | 1.018                          | -0.030          | -0.031                          | 3862.3                 |
| 149               | AGTCAGATCCCTACATCAAAA               | 293        | 55.78                       | 1.30   | -0.673               | 1.018                          | -0.030          | -0.030                          | 2869.9                 |
| 150               | GTCAATCTCTACATCAAAAT                | 294        | 55.62                       | 1.70   | -0.697               | 1.366                          | 0.087           | -0.089                          | 3542.9                 |
| 151               | TGAGATCTCTACATCAAAATC               | 295        | 54.02                       | 1.50   | -0.932               | 1.192                          | -0.125          | -0.122                          | 2477.1                 |
| 152               | AGATCTCTCTACATCAAAATCA              | 296        | 54.07                       | 1.10   | -0.924               | 0.844                          | -0.252          | -0.041                          | 2522.4                 |
| 153               | AGATCTCTCTACATCAAAATCAT             | 297        | 52.83                       | 1.10   | -1.106               | 0.844                          | -0.365          | -0.046                          | 2554.6                 |
| 154               | GATCTCTCTACATCAAAATCATC             | 298        | 53.87                       | 1.50   | -0.953               | 1.192                          | -0.138          | -0.031                          | 3580.0                 |
| 155               | ATCTCTCTCTACATCAAAATCATCC           | 299        | 56.33                       | 1.80   | -0.591               | 1.453                          | 0.185           | -0.062                          | 5937.7                 |
| 156               | TCTCTCTCTCTACATCAAAATCATCCA         | 300        | 57.54                       | 1.80   | -0.415               | 1.453                          | 0.295           | -0.111                          | 4806.7                 |
| 157               | CTCTCTCTCTCTACATCAAAATCATCCAT       | 301        | 56.32                       | 1.80   | -0.594               | 1.453                          | 0.184           | -0.159                          | 4877.2                 |
| 158               | CTCTCTCTCTCTCTACATCAAAATCATCCATG    | 302        | 52.68                       | 1.10   | -1.128               | 0.844                          | -0.379          | -0.228                          | 2608.6                 |
| 159               | TCTCTCTCTCTCTCTCTACATCAAAATCATCCCTG | 303        | 53.56                       | 0.30   | -0.999               | 0.149                          | -0.563          | -0.469                          | 1491.7                 |
| 160               | ACATCAAAATCATCAATCATCTA             | 304        | 53.56                       | -0.10  | -0.999               | -0.199                         | -0.695          | -0.644                          | 1364.3                 |
| 161               | CATCAAAATCATCAATCATAT               | 305        | 53.07                       | -0.80  | -0.071               | -0.808                         | -0.971          | -0.751                          | 1089.8                 |

Table 4

| p5 Probe Position | DNA Probe Sequence          | SEQ ID NO: | RNA/DNA T <sub>m</sub> (°C) | $\Delta G_{fold}$ (kcal/mole @ 35 °C) | T <sub>m</sub> Score | $\Delta G_{fold}$ Score | Composite Score | Window-Averaged Composite Score | HIV PRT GeneChip™ Data |
|-------------------|-----------------------------|------------|-----------------------------|---------------------------------------|----------------------|-------------------------|-----------------|---------------------------------|------------------------|
| 162               | ATACAAATCATCCATGATT         | 306        | 52.11                       | -1.10                                 | -1.211               | -1.089                  | -1.157          | -0.878                          | 1008.6                 |
| 163               | TACAAATCATCCNGATTTG         | 307        | 52.08                       | -0.40                                 | -1.215               | -0.480                  | -0.928          | -0.891                          | 624.8                  |
| 164               | ACAAATCATCCATGATTTGA        | 308        | 53.86                       | 0.20                                  | -0.955               | 0.082                   | -0.568          | -0.921                          | 535.8                  |
| 165               | CAAAATCATCCATGATTGAT        | 309        | 53.36                       | -0.50                                 | -1.027               | -0.547                  | -0.845          | -0.860                          | 3019.6                 |
| 166               | AAATCATCATCATGATTGATA       | 310        | 51.57                       | -0.70                                 | -1.291               | -1.074                  | -0.901          | -0.753                          | 214.0                  |
| 167               | AATCATCATCATGATTGATG        | 311        | 53.47                       | -0.70                                 | -1.012               | -0.721                  | -0.901          | -0.685                          | 212.7                  |
| 168               | ATCATCATCATGATTGATAGA       | 312        | 56.66                       | -0.50                                 | -0.543               | -0.547                  | -0.545          | -0.709                          | 165.2                  |
| 169               | TCATCCATGATTGATTGATG        | 313        | 56.66                       | -0.10                                 | -0.543               | -0.199                  | -0.412          | -0.686                          | 166.0                  |
| 170               | CATCCATGATTGATTGATAGA       | 314        | 54.80                       | 0.30                                  | -0.817               | 0.149                   | -0.450          | -0.622                          | 151.0                  |
| 171               | ATCCATGATTGATTGATGATA       | 315        | 51.69                       | 0.30                                  | -1.273               | 0.149                   | -0.733          | -0.621                          | 101.8                  |
| 172               | TCATCATGATTGATTGATTAAC      | 316        | 52.19                       | 0.30                                  | -1.199               | 0.149                   | -0.887          | -0.721                          | 84.0                   |
| 173               | CAATGATTGATTGATTGATTAAC     | 317        | 52.89                       | 0.30                                  | -1.097               | 0.149                   | -0.623          | -0.850                          | 130.3                  |
| 174               | CATGTAATGATTGATTGATTAAC     | 318        | 48.47                       | 0.70                                  | -1.746               | 0.496                   | -0.894          | -0.937                          | 67.8                   |
| 175               | ATGTAATGATTGATTGATTGATTAAC  | 319        | 47.12                       | 0.00                                  | -1.944               | -0.112                  | -1.248          | -1.006                          | 65.7                   |
| 176               | TGTAATGATTGATTGATTGATTAAC   | 320        | 47.11                       | -0.20                                 | -1.945               | -0.286                  | -1.315          | -1.048                          | 90.0                   |
| 177               | GTATGATTGATTGATTGATTGATTAAC | 321        | 49.90                       | -0.20                                 | -1.536               | -0.286                  | -1.061          | -1.099                          | 125.9                  |
| 178               | TATTGATTGATTGATTGATTGATTAAC | 322        | 48.24                       | -0.20                                 | -1.779               | -0.286                  | -1.212          | -1.083                          | 132.6                  |
| 179               | ATGTAATGATTGATTGATTGATTAAC  | 323        | 50.78                       | -0.20                                 | -1.407               | -0.286                  | -0.981          | -0.998                          | 167.4                  |
| 180               | TGTAATGATTGATTGATTGATTAAC   | 324        | 50.75                       | -0.20                                 | -1.411               | -0.286                  | -0.984          | -0.976                          | 219.0                  |
| 181               | TGATGATTGATTGATTGATTGATTAAC | 325        | 53.01                       | -0.20                                 | -1.080               | -0.286                  | -0.778          | -0.866                          | 722.6                  |
| 182               | GATGATTGATTGATTGATTGATTAAC  | 326        | 54.36                       | -0.20                                 | -0.881               | -0.286                  | -0.655          | -0.774                          | 825.1                  |
| 183               | TATGATTGATTGATTGATTGATTAAC  | 327        | 53.04                       | -0.10                                 | -1.074               | -0.199                  | -0.742          | -0.629                          | 844.4                  |
| 184               | TATGATTGATTGATTGATTGATTAAC  | 328        | 53.37                       | -0.10                                 | -1.027               | -0.199                  | -0.712          | -0.569                          | 912.6                  |
| 185               | AGATGATTGATTGATTGATTGATTAAC | 329        | 54.27                       | 0.10                                  | -0.895               | -0.025                  | -0.565          | -0.449                          | 1301.8                 |
| 186               | GATGATTGATTGATTGATTGATTAAC  | 330        | 54.43                       | 0.80                                  | -0.870               | 0.583                   | -0.318          | -0.335                          | 1367.4                 |
| 187               | ATGATTGATTGATTGATTGATTAAC   | 331        | 53.08                       | 1.50                                  | -1.070               | 1.192                   | -0.210          | -0.172                          | 1284.2                 |
| 188               | TACTGATTGATTGATTGATTAAC     | 332        | 56.05                       | 1.50                                  | -0.634               | 1.192                   | 0.060           | -0.026                          | 1162.5                 |

Table 4

| p5 Probe Position | DNA Probe Sequence   | SEQ ID NO: | RNA/DNA T <sub>m</sub> (°C) | $\Delta G_{\text{fold}}$ (kcal/mole @ 35 °C) | T <sub>m</sub> Score | $\Delta G_{\text{fold}}$ Score | Composite Score | Window-Averaged Composite Score | HIV PRT GeneChip™ Data |
|-------------------|----------------------|------------|-----------------------------|--|----------------------|--------------------------------|-----------------|---------------------------------|------------------------|
| 188               | ACTATGCTCGGATTTGTT   | 333        | 56.97                       | 1.50   | -0.499               | 1.192                          | 0.144           | 0.084                           | 1396.7                 |
| 190               | ACTATGCTCGGATTTGTT   | 334        | 59.38                       | 1.50   | -0.145               | 1.192                          | 0.363           | 0.176                           | 1348.3                 |
| 191               | CTATGCTCGGATTTGTTT   | 335        | 59.16                       | 1.50   | -0.171               | 1.192                          | 0.343           | 0.261                           | 1092.8                 |
| 192               | TATGCTCGGATTTGTTT    | 336        | 57.45                       | 1.50   | -0.428               | 1.192                          | 0.188           | 0.234                           | 912.6                  |
| 193               | ATGCTCGGATTTGTTT     | 337        | 58.41                       | 1.70   | -0.287               | 1.366                          | 0.341           | 0.123                           | 994.3                  |
| 194               | TGCTCGGATTTGTTTTA    | 338        | 57.81                       | 2.00   | -0.375               | 1.627                          | 0.386           | -0.079                          | 840.7                  |
| 195               | CTCGGATTTGTTTTAA     | 339        | 55.82                       | 1.00   | -0.667               | 0.757                          | -0.126          | -0.344                          | 941.9                  |
| 196               | CTCGGATTTGTTTTAA     | 340        | 50.98                       | 0.80   | -1.377               | 0.583                          | -0.632          | -0.488                          | 84.9                   |
| 197               | CTCGATTTGTTTTAAAA    | 341        | 48.16                       | 0.30   | -1.790               | 0.149                          | -1.054          | -0.670                          | 78.6                   |
| 198               | TGGAATTTGTTTTAAAG    | 342        | 46.41                       | 0.10   | -2.048               | -0.025                         | -1.279          | -0.851                          | 93.2                   |
| 199               | GGATTTGTTTTAAAGG     | 343        | 48.87                       | 0.10   | -1.686               | -0.025                         | -1.055          | -0.933                          | 56.0                   |
| 200               | GATTTGTTTTAAAGGC     | 344        | 50.22                       | 0.10   | -1.488               | -0.025                         | -0.932          | -0.912                          | 49.9                   |
| 201               | ATTGTTTTTAAAGGCT     | 345        | 50.84                       | 0.10   | -1.397               | -0.025                         | -0.876          | -0.843                          | 55.0                   |
| 202               | TTTGTTTTTAAAGGCTC    | 346        | 52.03                       | 0.30   | -1.223               | 0.149                          | -0.702          | -0.768                          | 64.6                   |
| 203               | TTTGTTTTTAAAGGCTCT   | 347        | 53.64                       | 0.50   | -0.987               | 0.323                          | -0.489          | -0.724                          | 162.8                  |
| 204               | TGTTTTTAAAGGCTCTA    | 348        | 52.76                       | 0.50   | -1.115               | 0.323                          | -0.569          | -0.706                          | 265.8                  |
| 205               | TGTTTTTAAAGGCTCTAA   | 349        | 50.71                       | 0.50   | -1.417               | 0.323                          | -0.756          | -0.672                          | 288.5                  |
| 206               | TTTTTTTAAAGGCTCTAAG  | 350        | 50.86                       | 0.50   | -1.395               | 0.323                          | -0.742          | -0.672                          | 548.4                  |
| 207               | TTTTTAAAGGCTCTAAGA   | 351        | 49.40                       | 0.70   | -1.609               | 0.496                          | -0.809          | -0.698                          | 524.7                  |
| 208               | TTTTTAAAGGCTCTAAGAT  | 352        | 49.11                       | 1.20   | -1.651               | 0.931                          | -0.670          | -0.746                          | 937.9                  |
| 209               | TTTTTAAAGGCTCTAAGATT | 353        | 49.11                       | 1.20   | -1.651               | 0.931                          | -0.670          | -0.790                          | 1440.3                 |
| 210               | TTTTTAAAGGCTCTAAGATT | 354        | 49.11                       | 1.20   | -1.651               | 0.931                          | -0.670          | -0.820                          | 1633.3                 |
| 211               | TTTAAAGGCTCTAAGATTTT | 355        | 49.11                       | 0.50   | -1.651               | 0.323                          | -0.901          | -0.735                          | 1987.4                 |
| 212               | TAAAGGCTCTAAGATTTT   | 356        | 49.11                       | 0.00   | -1.651               | -0.112                         | -1.067          | -0.622                          | 1792.3                 |
| 213               | AAAGGCTCTAAGATTTTG   | 357        | 49.63                       | 0.20   | -1.575               | 0.062                          | -0.953          | -0.495                          | 2218.9                 |
| 214               | AAGGCTCTAAGATTTTGT   | 358        | 54.13                       | 1.20   | -0.914               | 0.931                          | -0.213          | -0.365                          | 2371.4                 |
| 215               | AAGGCTCTAAGATTTGTCT  | 359        | 57.38                       | 1.20   | -0.439               | 0.931                          | 0.082           | -0.238                          | 3308.9                 |

Table 4

| p5 Probe Position | DNA Probe Sequence     | SEQ ID NO: | RNA/DNA $T_m$ (°C) | $\Delta G_{\text{Mfold}}$ (kcal/mole @ 35 °C) | $T_m$ Score | $\Delta G_{\text{Mfold}}$ Score | Composite Score | Window-Averaged Composite Score | HIV PRT GeneChip™ Data |
|-------------------|------------------------|------------|--------------------|---|-------------|---------------------------------|-----------------|---------------------------------|------------------------|
| 216               | AGGCTCTAAGATTTTGTGCA   | 360        | 60.78              | 0.80  | 0.061       | 0.583                           | 0.260           | -0.082                          | 4070.5                 |
| 217               | GGCTCTAAGATTTTGTGCAT   | 361        | 60.56              | 0.80  | 0.028       | 0.583                           | 0.239           | 0.048                           | 5394.5                 |
| 218               | GGCTCTAAGATTTTGTGACG   | 362        | 57.81              | 0.80  | -0.376      | 0.583                           | -0.011          | 0.064                           | 2025.5                 |
| 219               | CTCTAAGATTTTGTGTGATG   | 363        | 57.81              | 0.80  | -0.376      | 0.583                           | -0.011          | -0.066                          | 1741.9                 |
| 220               | CTCTAAGATTTTGTGTGATG   | 364        | 57.81              | 0.80  | -0.376      | 0.583                           | -0.011          | -0.066                          | 1707.6                 |
| 221               | CTAAGATTTTGTGTGATGCTA  | 365        | 55.87              | 0.80  | -0.660      | 0.583                           | -0.187          | -0.088                          | 1783.0                 |
| 222               | TAAGATTTTGTGTGATGCTAC  | 366        | 54.43              | 0.80  | -0.872      | 0.583                           | -0.319          | -0.076                          | 3131.4                 |
| 223               | AGATTTTGTGTGATGCTACT   | 367        | 56.99              | 0.80  | -0.495      | 0.410                           | -0.151          | -0.082                          | 4892.5                 |
| 224               | AGATTTTGTGTGATGCTACT   | 368        | 59.39              | 0.80  | -0.144      | 0.410                           | 0.067           | -0.063                          | 5856.4                 |
| 225               | GATTTTGTGTGATGCTACTTT  | 369        | 59.54              | 0.80  | -0.122      | 0.410                           | 0.080           | 0.046                           | 6439.0                 |
| 226               | ATTTTGTGTGATGCTACTTTG  | 370        | 58.09              | 0.80  | -0.334      | 0.410                           | -0.051          | 0.069                           | 5820.3                 |
| 227               | TTTGTGTGATGCTACTTTGG   | 371        | 60.78              | 0.80  | 0.060       | 0.410                           | 0.193           | 0.096                           | 5189.6                 |
| 228               | TTTGTGTGATGCTACTTTGGA  | 372        | 61.79              | 0.80  | 0.209       | 0.410                           | 0.285           | 0.079                           | 4721.7                 |
| 229               | TTTGTGTGATGCTACTTTGGAA | 373        | 59.35              | 0.80  | -0.149      | 0.410                           | 0.063           | 0.075                           | 4221.0                 |
| 230               | TTTGTGTGATGCTACTTTGGAA | 374        | 59.00              | 0.80  | -0.200      | 0.410                           | 0.032           | 0.066                           | 4279.0                 |
| 231               | TGTGTGATGCTACTTTGGAA   | 375        | 58.10              | 0.80  | -0.333      | 0.410                           | -0.051          | 0.004                           | 4102.0                 |
| 232               | GTCGTGATGCTACTTTGGAA   | 376        | 58.16              | 0.80  | -0.324      | 0.670                           | 0.054           | -0.022                          | 5069.8                 |
| 233               | TCATGCTACTTTGGAAATTT   | 377        | 55.52              | 0.90  | -0.711      | 0.670                           | -0.186          | -0.045                          | 2407.9                 |
| 234               | CATGCTACTTTGGAAATTTG   | 378        | 54.23              | 1.30  | -0.900      | 1.018                           | -0.171          | 0.046                           | 2443.0                 |
| 235               | ATGCTACTTTGGAAATTTGTC  | 379        | 56.90              | 1.40  | -0.508      | 1.105                           | 0.105           | 0.058                           | 2324.3                 |
| 236               | GCTACTTTGGAAATTTGCT    | 380        | 58.82              | 0.90  | -0.227      | 0.670                           | 0.114           | 0.099                           | 1894.1                 |
| 237               | GCTACTTTGGAAATTTGCTG   | 381        | 58.82              | 1.30  | -0.227      | 1.018                           | 0.246           | 0.190                           | 2363.0                 |
| 238               | CTACTTTGGAAATTTGCTGG   | 382        | 57.35              | 1.70  | -0.443      | 1.366                           | 0.244           | 0.270                           | 1363.8                 |
| 239               | TACTTTGGAAATTTGCTGGT   | 383        | 58.39              | 1.70  | -0.290      | 1.366                           | 0.339           | 0.299                           | 1211.5                 |
| 240               | ACTTTGGAAATTTGCTGGTG   | 384        | 58.88              | 1.70  | -0.217      | 1.366                           | 0.384           | 0.340                           | 1621.8                 |
| 241               | CTTTGGAAATTTGCTGGTGA   | 385        | 59.64              | 1.70  | -0.106      | 1.366                           | 0.384           | 0.346                           | 1432.2                 |
| 242               | TTTGGAAATTTGCTGGTAT    | 386        | 57.72              | 1.80  | -0.388      | 1.453                           | 0.311           | 0.345                           | 1608.0                 |

Table 4

| p5 Probe Position | DNA Probe Sequence    | SEQ ID NO: | RNA/DNA T <sub>m</sub> (°C) | $\Delta G_{\text{fold}}$ (kcal/mole @ 35 °C) | T <sub>m</sub> Score | $\Delta G_{\text{fold}}$ Score | Composite Score | Window-Averaged Composite Score | HIV PRT GeneChip™ Data |
|-------------------|-----------------------|------------|-----------------------------|--|----------------------|--------------------------------|-----------------|---------------------------------|------------------------|
| 243               | TTGGAATATTCGTGGTATC   | 387        | 58.73                       | 1.80   | -0.241               | 1.453                          | 0.403           | 0.302                           | 2334.6                 |
| 244               | TGGAAATATTCGTGGTATCC  | 388        | 62.18                       | 0.50   | 0.266                | 0.323                          | 0.288           | 0.344                           | 3776.7                 |
| 245               | GGAAATATTCGTGGTATCCT  | 389        | 64.19                       | -0.20  | 0.561                | -0.286                         | 0.239           | 0.246                           | 5848.7                 |
| 246               | GAATATTCGTGGTATTCCTT  | 390        | 61.99                       | -0.20  | 0.238                | -0.286                         | 0.039           | 0.264                           | 5358.8                 |
| 247               | AATATTCGTGGTATTCCTTT  | 391        | 61.03                       | -0.20  | 0.097                | -0.286                         | -0.049          | 0.446                           | 5517.2                 |
| 248               | ATATTCGTGGTATTCCTTTC  | 392        | 64.63                       | -0.20  | 0.825                | -0.286                         | 0.279           | 0.368                           | 6246.4                 |
| 249               | TATTCGTGGTATTCCTTTCC  | 393        | 68.48                       | -0.20  | 1.190                | -0.286                         | 0.629           | 0.444                           | 9975.1                 |
| 250               | ATTCGTGGTATTCCTTTCCA  | 394        | 70.22                       | -0.20  | 1.446                | -0.286                         | 0.788           | 0.599                           | 11990.0                |
| 251               | TGCTGGTATTCCTTTTCAT   | 395        | 70.22                       | -0.60  | 1.446                | -0.634                         | 0.655           | 0.756                           | 11843.0                |
| 252               | TGCTGGTATTCCTTTTCATC  | 396        | 71.48                       | -0.60  | 1.631                | -0.634                         | 0.770           | 0.862                           | 14125.0                |
| 253               | GCTGGTATTCCTTTTCATCC  | 397        | 75.32                       | -0.60  | 2.193                | -0.634                         | 1.119           | 0.936                           | 23489.0                |
| 254               | CTGGTATTCCTTTTCATCCC  | 398        | 74.58                       | -0.60  | 2.085                | -0.634                         | 1.052           | 1.022                           | 15975.0                |
| 255               | TGGTATTCCTTTTCATCCCT  | 399        | 74.58                       | -0.70  | 2.085                | -0.721                         | 1.019           | 1.082                           | 16053.0                |
| 256               | GGTATTCCTTTTCATCCCTG  | 400        | 74.58                       | -0.30  | 2.085                | -0.373                         | 1.151           | 1.136                           | 19205.0                |
| 257               | GTGATTCCTTTTCATCCCTGT | 401        | 75.40                       | 0.20   | 2.206                | 0.062                          | 1.391           | 1.080                           | 17872.0                |
| 258               | TGATTCCTTTTCATCCCTGTG | 402        | 71.89                       | 0.20   | 1.691                | 0.062                          | 1.072           | 0.955                           | 12871.0                |
| 259               | GATTCCTTTTCATCCCTGTGG | 403        | 74.58                       | -0.30  | 2.085                | -0.373                         | 1.151           | 0.809                           | 8792.7                 |
| 260               | ATTCCTTTTCATCCCTGTGGA | 404        | 74.58                       | -1.60  | 2.085                | -1.504                         | 0.721           | 0.653                           | 5609.6                 |
| 261               | TCTTCATCCCTGTGGAA     | 405        | 72.27                       | -2.80  | 1.746                | -2.373                         | 0.181           | 0.451                           | 3018.0                 |
| 262               | CTTCATCCCTGTGGAG      | 406        | 71.00                       | -2.80  | 1.559                | -2.547                         | -0.001          | 0.308                           | 1802.6                 |
| 263               | CTTCATCCCTGTGGAGC     | 407        | 71.60                       | -2.80  | 1.648                | -2.547                         | 0.054           | 0.205                           | 1074.0                 |
| 264               | TTTCATCCCTGTGGAGCA    | 408        | 70.81                       | -2.80  | 1.532                | -2.547                         | -0.018          | 0.120                           | 1132.5                 |
| 265               | TTCATCCCTGTGGAGCAC    | 409        | 71.02                       | -2.60  | 1.562                | -2.373                         | 0.067           | 0.024                           | 1454.5                 |
| 266               | TCATCCCTGTGGAGCAC     | 410        | 71.74                       | -1.70  | 1.669                | -1.591                         | 0.307           | 0.032                           | 1678.8                 |
| 267               | CAATCCCTGTGGAGCACAT   | 411        | 70.20                       | -2.20  | 1.443                | -2.025                         | 0.430           | 0.006                           | 2268.9                 |
| 268               | CAATCCCTGTGGAGCACAT   | 412        | 67.07                       | -2.20  | 0.983                | -2.025                         | -0.160          | 0.004                           | 1682.6                 |
| 269               | ATCCCTGTGGAGCACATG    | 413        | 65.82                       | -2.20  | 0.801                | -2.025                         | -0.273          | -0.070                          | 1753.9                 |

Table 4

| p5 Probe Position | DNA Probe Sequence    | SEQ ID NO: | RNA/DNA T <sub>m</sub> (°C) | $\Delta G_{\text{Mfold}}$ (kcal/mole @ 35 °C) | T <sub>m</sub> Score | $\Delta G_{\text{Mfold}}$ Score | Composite Score | Window-Averaged Composite Score | HIV PRT GeneChip™ Data |
|-------------------|-----------------------|------------|-----------------------------|---|----------------------|---------------------------------|-----------------|---------------------------------|------------------------|
| 270               | TCCTGTGGAGACACATGT    | 414        | 68.98                       | -2.20   | 1.263                | -2.025                          | 0.014           | -0.320                          | 1281.8                 |
| 271               | CCCTGTGGAGACACATGTA   | 415        | 66.92                       | -2.20   | 0.962                | -2.025                          | -0.173          | -0.344                          | 1227.8                 |
| 272               | CTGTGTGGAGACACATGTAC  | 416        | 63.84                       | -2.20   | 0.509                | -2.025                          | -0.454          | -0.332                          | 700.3                  |
| 273               | CTGTGTGGAGACATGTACT   | 417        | 62.01                       | -2.20   | 0.241                | -2.025                          | -0.620          | -0.302                          | 618.7                  |
| 274               | CTGTGTGGAGACATGTACTG  | 418        | 59.99                       | -2.00   | -0.056               | -1.851                          | -0.738          | -0.324                          | 771.5                  |
| 275               | TGTGAAGACACATGTACTGA  | 419        | 61.39                       | -0.50   | 0.149                | -0.547                          | -0.115          | -0.342                          | 1180.6                 |
| 276               | TGTGAAGACACATGTACTGAT | 420        | 58.35                       | 0.50  | -0.296               | 0.323                           | -0.061          | -0.331                          | 1160.5                 |
| 277               | GGAGACACATGTACTAGTAT  | 421        | 57.86                       | 0.50  | -0.368               | 0.323                           | -0.106          | -0.339                          | 1314.7                 |
| 278               | GAAGACATGTACTAGTAT    | 422        | 55.32                       | 0.50  | -0.740               | 0.323                           | -0.336          | -0.341                          | 1102.5                 |
| 279               | AGACACATGTACTAGTATC   | 423        | 55.30                       | 0.50  | -0.744               | 0.323                           | -0.339          | -0.300                          | 1222.1                 |
| 280               | AGCACATGTACTAGTATCT   | 424        | 59.26                       | 0.50  | -0.162               | 0.323                           | 0.022           | -0.302                          | 1893.2                 |
| 281               | GCACATGTACTAGTATCTA   | 425        | 58.48                       | 0.50  | -0.277               | 0.323                           | -0.049          | -0.398                          | 2097.7                 |
| 282               | CACATGTACTAGTATCTMA   | 426        | 52.51                       | 0.50  | -1.152               | 0.323                           | -0.592          | -0.446                          | 1237.8                 |
| 283               | ACATGTACTAGTATCTAAT   | 427        | 51.20                       | 0.50  | -1.345               | 0.323                           | -0.711          | -0.443                          | 959.5                  |
| 284               | CATGTACTAGTATCTAATC   | 428        | 51.89                       | 0.10  | -1.244               | -0.025                          | -0.781          | -0.472                          | 1149.1                 |
| 285               | ATGTACTAGTATCTAATCC   | 429        | 54.53                       | -0.30   | -0.856               | -0.373                          | -0.672          | -0.490                          | 2351.3                 |
| 286               | TGTACTAGTATCTAATCCC   | 430        | 58.41                       | -0.30   | -0.287               | -0.373                          | -0.320          | -0.436                          | 4191.6                 |
| 287               | TGTACTAGTATCTAATCCCT  | 431        | 59.99                       | -0.30   | -0.055               | -0.373                          | -0.176          | -0.320                          | 5565.8                 |
| 288               | GTACTAGTATCTAATCCG    | 432        | 59.99                       | -0.30   | -0.055               | -0.373                          | -0.176          | -0.320                          | 5565.8                 |
| 289               | TACTAGTATCTAATCCCTG   | 433        | 59.52                       | -0.30   | -0.124               | -0.373                          | -0.218          | -0.302                          | 9980.2                 |
| 290               | ACTGATATCTAATCCCTGGT  | 434        | 63.07                       | -0.30   | 0.397                | -0.373                          | 0.104           | 0.023                           | 7749.5                 |
| 291               | CTGATATCTAATCCCTGGTG  | 435        | 62.43                       | -0.30   | 0.303                | -0.373                          | 0.046           | 0.184                           | 8165.3                 |
| 292               | TGATATCTAATCCCTGGTGT  | 436        | 63.60                       | -0.30   | 0.474                | -0.373                          | 0.152           | 0.365                           | 9107.6                 |
| 293               | GATATCTAATCCCTGGTGTC  | 437        | 65.19                       | 0.10  | 0.707                | -0.025                          | 0.429           | 0.566                           | 13914.0                |
| 294               | ATATCTAATCCCTGGTGTC   | 438        | 65.82                       | 1.50  | 0.900                | 1.192                           | 0.949           | 0.698                           | 15093.0                |
| 295               | TATCTAATCCCTGGTGTC    | 439        | 67.41                       | 1.50  | 1.033                | 1.192                           | 1.093           | 0.822                           | 18647.0                |
| 296               | ATCTAATCCCTGGTGTC     | 440        | 69.20                       | 1.30  | 1.296                | 1.018                           | 1.190           | 0.904                           | 21810.0                |

Table 4

| p5 Probe Position | DNA Probe Sequence  | SEQ ID NO. | RNA/DNA T <sub>m</sub> (°C) | $\Delta G_{\text{Mfold}}$ (kcal/mole @ 35°C) | T <sub>m</sub> Score | $\Delta G_{\text{Mfold}}$ Score | Composite Score | Window-Averaged Composite Score | HIV PRT GeneChip™ Data |
|-------------------|---------------------|------------|-----------------------------|--|----------------------|---------------------------------|-----------------|---------------------------------|------------------------|
| 297               | TCTAATCCCTGGTCTCAT  | 441        | 69.20                       | 0.80   | 1.296                | 0.583                           | 1.025           | 0.996                           | 20102.0                |
| 298               | CTAATCCCTGGTGTCTCAT | 442        | 67.98                       | 0.80   | 1.117                | 0.583                           | 0.914           | 1.052                           | 20967.0                |
| 299               | TAATCCCTGGTGTCTCAT  | 443        | 65.90                       | 0.80   | 0.811                | 0.583                           | 0.725           | 1.092                           | 18200.0                |
| 300               | AATCCCTGGTGTCTCAT   | 444        | 68.78                       | 0.80   | 1.380                | 0.583                           | 1.077           | 1.088                           | 19845.0                |
| 301               | ATCCCTGGTGTCTCAT    | 445        | 72.61                       | 0.80   | 1.797                | 0.583                           | 1.336           | 1.057                           | 19231.0                |
| 302               | CCCTGGTGTCTCAT      | 446        | 73.04                       | 0.80   | 1.860                | 0.583                           | 1.375           | 0.981                           | 17629.0                |
| 303               | CCCTGGTGTCTCAT      | 447        | 70.72                       | 0.80   | 1.519                | 0.583                           | 1.164           | 0.918                           | 17009.0                |
| 304               | CTGGTGTCTCAT        | 448        | 66.82                       | 0.80   | 0.946                | 0.583                           | 0.808           | 0.900                           | 11560.0                |
| 305               | CTGGTGTCTCAT        | 449        | 62.17                       | 0.80   | 0.264                | 0.583                           | 0.386           | 0.600                           | 8374.6                 |
| 306               | TGGTGTCTCAT         | 450        | 60.65                       | 0.90   | 0.042                | 0.670                           | 0.281           | 0.355                           | 6153.3                 |
| 307               | GGTGTCTCAT          | 451        | 62.88                       | 0.20   | 0.369                | 0.062                           | 0.252           | 0.172                           | 7134.0                 |
| 308               | GTGTCTCAT           | 452        | 59.43                       | 0.20   | -0.138               | 0.062                           | -0.082          | 0.050                           | 4435.2                 |
| 309               | GTCTCAT             | 453        | 56.35                       | 0.20   | -0.589               | 0.062                           | -0.342          | -0.043                          | 2035.5                 |
| 310               | GTCAT               | 454        | 59.21                       | 0.20   | -0.170               | 0.062                           | -0.082          | -0.149                          | 2466.6                 |
| 311               | TCTCAT              | 455        | 59.21                       | 0.20   | -0.170               | 0.062                           | -0.082          | -0.268                          | 1080.9                 |
| 312               | CTCAT               | 456        | 57.15                       | 0.20   | -0.472               | 0.062                           | -0.269          | -0.325                          | 956.0                  |
| 313               | TCAT                | 457        | 55.08                       | 0.20   | -0.776               | 0.062                           | -0.458          | -0.302                          | 529.4                  |
| 314               | CTTTTACTAGTATG      | 458        | 53.70                       | 0.20   | -0.978               | 0.062                           | -0.583          | -0.328                          | 471.4                  |
| 315               | ATTGTTTACTAGTATG    | 459        | 55.01                       | 0.20   | -0.785               | 0.062                           | -0.463          | -0.340                          | 510.4                  |
| 316               | TGTTTACTAGTATG      | 460        | 58.17                       | 0.20   | -0.322               | 0.062                           | -0.176          | -0.486                          | 531.0                  |
| 317               | TGTTTACTAGTATG      | 461        | 57.21                       | 0.20   | -0.463               | 0.062                           | -0.264          | -0.660                          | 613.3                  |
| 318               | GTTTACTAGTATG       | 462        | 55.23                       | 0.00   | -0.753               | -0.112                          | -0.510          | -0.620                          | 685.1                  |
| 319               | TTTACTAGTATG        | 463        | 50.42                       | 0.00   | -1.459               | -0.112                          | -0.947          | -0.636                          | 300.0                  |
| 320               | TATCTAGTATG         | 464        | 50.12                       | 0.00   | -1.504               | -0.112                          | -0.975          | -0.632                          | 316.1                  |
| 321               | TATCTAGTATG         | 465        | 48.79                       | 0.00   | -1.551               | -0.112                          | -1.004          | -0.655                          | 387.5                  |
| 322               | ATCTAGTATG          | 466        | 54.30                       | 0.00   | -0.889               | -0.112                          | -0.584          | -0.652                          | 685.7                  |
| 323               | TACTAGTATG          | 467        | 55.59                       | 0.20   | -0.700               | 0.062                           | -0.411          | -0.430                          | 759.6                  |

Table 4

| p5 Probe Position | DNA Probe Sequence  | SEQ ID NO: | RNA/DNA T <sub>m</sub> (°C) | $\Delta G_{\text{Mfold}}$ (kcal/mole @ 35 °C) | T <sub>m</sub> Score | $\Delta G_{\text{Mfold}}$ Score | Composite Score | Window-Averaged Composite Score | HIV PRT GeneChip™ Data |
|-------------------|---------------------|------------|-----------------------------|---|----------------------|---------------------------------|-----------------|---------------------------------|------------------------|
| 324               | ACTAGGTATGTTAAATGCG | 468        | 56.32                       | 0.80  | -0.593               | 0.583                           | -0.146          | -0.294                          | 1050.2                 |
| 325               | CTAGGTATGTTAAATGCGT | 469        | 58.78                       | 1.10  | -0.232               | 0.844                           | 0.177           | -0.152                          | 1020.4                 |
| 326               | TAGGTATGTTAAATGCGT  | 470        | 56.24                       | 1.10  | -0.605               | 0.844                           | -0.054          | -0.100                          | 742.6                  |
| 327               | AGGTATGTTAAATGCGTAT | 471        | 56.81                       | 1.10  | -0.521               | 0.844                           | -0.002          | -0.132                          | 889.6                  |
| 328               | TGATGTTAAATGCGTAT   | 472        | 56.07                       | 1.10  | -0.631               | 0.844                           | -0.070          | -0.182                          | 858.8                  |
| 329               | GTATGTTAAATGCGTATAC | 473        | 54.02                       | 1.10  | -0.931               | 0.844                           | -0.256          | -0.262                          | 379.0                  |
| 330               | TATGTTAAATGCGTATCT  | 474        | 53.06                       | 0.40  | -1.071               | 0.236                           | -0.575          | -0.252                          | 166.7                  |
| 331               | ATGTTAAATGCGTATCTCT | 475        | 53.94                       | 0.40  | -0.943               | 0.236                           | -0.495          | -0.249                          | 215.3                  |
| 332               | TGTTAAATGCGTATCTTC  | 476        | 55.21                       | 0.40  | -0.757               | 0.236                           | -0.380          | -0.303                          | 103.2                  |
| 333               | GTAAATGCGTATCTTCC   | 477        | 59.15                       | 0.40  | -0.178               | 0.236                           | -0.021          | -0.326                          | 246.3                  |
| 334               | GTAAATGCGTATCTTCT   | 478        | 58.53                       | 0.80  | -0.269               | 0.583                           | 0.055           | -0.303                          | 163.4                  |
| 335               | TAAATGCGTATCTTCTCG  | 479        | 55.54                       | 0.10  | -0.708               | -0.025                          | -0.448          | -0.264                          | 294.1                  |
| 336               | AAATGCGTATCTTCTCGA  | 480        | 57.36                       | -0.30   | -0.441               | -0.373                          | -0.415          | -0.229                          | 531.4                  |
| 337               | AATGCGTATCTTCTGAA   | 481        | 57.36                       | -0.30   | -0.441               | -0.373                          | -0.415          | -0.233                          | 1995.5                 |
| 338               | ATGCGTATCTTCTGGA    | 482        | 59.50                       | -0.30   | -0.128               | -0.373                          | -0.221          | -0.279                          | 510.1                  |
| 339               | TGCGTATCTTCTGGAAT   | 483        | 62.63                       | -0.90   | 0.332                | -0.895                          | -0.134          | -0.264                          | 555.4                  |
| 340               | GCAGTATCTTCTGGAATC  | 484        | 64.24                       | -1.10   | 0.568                | -1.069                          | -0.054          | -0.238                          | 1214.0                 |
| 341               | CAGTATCTTCTGGAATCT  | 485        | 61.94                       | -1.10   | 0.230                | -1.069                          | -0.263          | -0.232                          | 825.7                  |
| 342               | AGTATCTTCTGGAATCTT  | 486        | 61.00                       | -1.10   | 0.094                | -1.069                          | -0.348          | -0.264                          | 1582.6                 |
| 343               | GTATCTTCTGGAATCTTC  | 487        | 62.28                       | -1.10   | 0.281                | -1.069                          | -0.232          | -0.278                          | 2391.8                 |
| 344               | TATCTTCTGGAATCTTCA  | 488        | 60.34                       | -1.10   | -0.004               | -1.069                          | -0.409          | -0.223                          | 2276.3                 |
| 345               | ATCTTCTGGAATCTTGAT  | 489        | 60.91                       | -1.20   | 0.080                | -1.156                          | -0.389          | -0.252                          | 2702.8                 |
| 346               | TCTTCTGGAATCTTCATC  | 490        | 62.40                       | -1.20   | 0.299                | -1.156                          | -0.254          | -0.274                          | 3781.7                 |
| 347               | CTTCTGGAATCTTCATCT  | 491        | 65.05                       | -1.20   | 0.886                | -1.156                          | -0.014          | -0.344                          | 5343.4                 |
| 348               | CTTCTGGAATCTTCATCTA | 492        | 63.86                       | -1.20   | 0.512                | -1.156                          | -0.122          | -0.344                          | 6309.0                 |
| 349               | TCTGGAATCTTCATCTAA  | 493        | 59.70                       | -1.20   | -0.098               | -1.156                          | -0.500          | -0.332                          | 6372.4                 |
| 350               | TCTGGAATCTTCATCTAAG | 494        | 59.55                       | -1.20   | -0.120               | -1.156                          | -0.513          | -0.369                          | 3835.3                 |

Table 4

| p5 Probe Position | DNA Probe Sequence   | SEQ ID NO: | RNA/DNA $T_m$ (°C) | $\Delta G_{\text{Mfold}}$ (kcal/mole @ 35 °C) | $T_m$ Score | $\Delta G_{\text{Mfold}}$ Score | Composite Score | Window-Averaged Composite Score | HIV PRT GeneChip™ Data |
|-------------------|----------------------|------------|--------------------|---|-------------|---------------------------------|-----------------|---------------------------------|------------------------|
| 351               | CTGAGCTCTTCATCTAAGG  | 495        | 60.76              | -1.20   | 0.057       | -1.156                          | -0.404          | -0.423                          | 8925.5                 |
| 352               | CTGAGCTCTTCATCTAAGG  | 496        | 59.48              | -1.20   | -0.130      | -1.156                          | -0.520          | -0.472                          | 1211.8                 |
| 353               | TGAAGCTCTTCATCTAAGGA | 497        | 58.84              | -1.00   | -0.224      | -0.982                          | -0.512          | -0.444                          | 609.4                  |
| 354               | GAGTCTTCATCTAAGGGAA  | 498        | 56.91              | -0.10   | -0.507      | -0.199                          | -0.390          | -0.358                          | 629.1                  |
| 355               | AGTCTTCATCTAAGGGAA   | 499        | 56.13              | -0.10   | -0.622      | -0.199                          | -0.461          | -0.341                          | 749.3                  |
| 356               | AGTCTTCATCTAAGGGA    | 500        | 60.12              | -0.10   | -0.036      | -0.199                          | -0.098          | -0.324                          | 805.6                  |
| 357               | GCTTCATCTAAGGGA      | 501        | 59.84              | -0.10   | -0.077      | -0.199                          | -0.124          | -0.449                          | 817.0                  |
| 358               | TCTTCATCTAAGGGA      | 502        | 58.11              | -0.10   | -0.331      | -0.199                          | -0.281          | -0.636                          | 327.1                  |
| 359               | CTTCATCTAAGGGA       | 503        | 54.95              | -0.60   | -0.794      | -0.634                          | -0.733          | -0.645                          | 320.0                  |
| 360               | TTTCATCTAAGGGA       | 504        | 51.39              | -0.80   | -1.316      | -0.634                          | -1.057          | -0.822                          | 84.1                   |
| 361               | CTTCATCTAAGGGA       | 505        | 49.50              | -0.10   | -1.595      | -0.025                          | -0.998          | -1.002                          | 67.7                   |
| 362               | CTTCATCTAAGGGA       | 506        | 46.98              | 0.10  | -1.963      | -0.025                          | -1.227          | -1.171                          | 62.2                   |
| 363               | ATCTAAGGGA           | 507        | 45.78              | 0.10  | -2.140      | -0.025                          | -1.336          | -1.298                          | 78.9                   |
| 364               | TCTAAGGGA            | 508        | 45.27              | 0.10  | -2.214      | -0.025                          | -1.382          | -1.328                          | 43.2                   |
| 365               | CTAAGGGA             | 509        | 44.36              | 0.10  | -2.349      | -0.025                          | -1.466          | -1.322                          | 50.4                   |
| 366               | TAAAGGGA             | 510        | 42.71              | 0.10  | -2.591      | -0.025                          | -1.616          | -1.242                          | 43.7                   |
| 367               | AAGGGA               | 511        | 46.54              | 0.10  | -2.028      | -0.025                          | -1.267          | -1.163                          | 45.6                   |
| 368               | AGGGA                | 512        | 49.21              | 0.30  | -1.637      | 0.149                           | -0.958          | -1.119                          | 49.8                   |
| 369               | GGGA                 | 513        | 49.11              | 1.20  | -1.651      | 0.931                           | -0.670          | -1.082                          | 53.2                   |
| 370               | GGA                  | 514        | 47.87              | 1.20  | -1.834      | 0.931                           | -0.783          | -0.958                          | 56.6                   |
| 371               | GA                   | 515        | 46.82              | 0.60  | -1.987      | 0.410                           | -1.076          | -0.844                          | 45.3                   |
| 372               | GA                   | 516        | 46.12              | 0.40  | -2.090      | 0.236                           | -1.206          | -0.773                          | 56.3                   |
| 373               | GA                   | 517        | 51.18              | 0.40  | -1.347      | 0.236                           | -0.746          | -0.703                          | 61.7                   |
| 374               | GA                   | 518        | 54.20              | 0.40  | -0.905      | 0.236                           | -0.471          | -0.646                          | 224.5                  |
| 375               | GA                   | 519        | 53.65              | 0.60  | -0.985      | 0.410                           | -0.455          | -0.446                          | 413.0                  |
| 376               | GA                   | 520        | 54.14              | 1.30  | -0.913      | 1.018                           | -0.179          | -0.289                          | 1584.0                 |
| 377               | GA                   | 521        | 54.14              | 1.30  | -0.913      | 1.018                           | -0.179          | -0.087                          | 1846.7                 |

Table 4

| p5 Probe Position | DNA Probe Sequence     | SEQ ID NO: | RNA/DNA T <sub>m</sub> (°C) | $\Delta G_{\text{fold}}$ (kcal/mole @ 35 °C) | T <sub>m</sub> Score | $\Delta G_{\text{fold}}$ Score | Composite Score | Window-Averaged Composite Score | HIV PRT GeneChip™ Data |
|-------------------|------------------------|------------|-----------------------------|--|----------------------|--------------------------------|-----------------|---------------------------------|------------------------|
| 378               | AAATATGTGATCACCACAT    | 522        | 55.78                       | 1.10   | -0.673               | 0.844                          | -0.096          | 0.966                           | 2445.8                 |
| 379               | AAATATGTGATCACCACATC   | 523        | 58.72                       | 0.90   | -0.241               | 0.670                          | 0.105           | 0.261                           | 3709.4                 |
| 380               | AAATATGATCACCACATCC    | 524        | 64.13                       | 0.90   | 0.552                | 0.670                          | 0.597           | 0.494                           | 4548.4                 |
| 381               | ATATGATCATCACCACATCCA  | 525        | 67.27                       | 0.90   | 1.013                | 0.670                          | 0.883           | 0.680                           | 5254.1                 |
| 382               | TATGATCATCACCACATCCG   | 526        | 67.53                       | 0.90   | 1.051                | 0.670                          | 0.906           | 0.864                           | 5527.2                 |
| 383               | ATGATCATCACCACATCCAGT  | 527        | 71.21                       | 0.90   | 1.590                | 0.670                          | 1.241           | 0.991                           | 6916.9                 |
| 384               | TGATCATCACCACATCCAGTA  | 528        | 70.68                       | 0.70   | 1.513                | 0.496                          | 1.127           | 1.030                           | 5861.4                 |
| 385               | GCATCACCACATCCAGTACT   | 529        | 71.39                       | 0.70   | 1.617                | 0.496                          | 1.191           | 1.043                           | 8078.4                 |
| 386               | CATCACCACATCCAGTACT    | 530        | 69.16                       | 0.70   | 1.290                | 0.496                          | 0.988           | 1.013                           | 4148.8                 |
| 387               | ATCACCACATCCAGTACTG    | 531        | 67.91                       | 0.70   | 1.107                | 0.496                          | 0.875           | 0.913                           | 3317.1                 |
| 388               | TCACCATCATCCAGTACTGT   | 532        | 71.15                       | 0.10   | 1.582                | -0.025                         | 0.971           | 0.830                           | 2486.4                 |
| 389               | CACCATCATCCAGTACTGTT   | 533        | 69.94                       | -0.40  | 1.404                | -0.460                         | 0.696           | 0.744                           | 2746.4                 |
| 390               | ACCATCATCCAGTACTGTTA   | 534        | 68.25                       | -0.40  | 1.157                | -0.460                         | 0.543           | 0.506                           | 2133.0                 |
| 391               | CCCATCATCCAGTACTGTTAC  | 535        | 68.25                       | -0.40  | 1.157                | -0.460                         | 0.543           | 0.392                           | 2197.0                 |
| 392               | CCCATCATCCAGTACTGTTACT | 536        | 66.50                       | -0.40  | 0.900                | -0.460                         | 0.383           | 0.666                           | 1824.0                 |
| 393               | CACATCCAGTACTGTTACTG   | 537        | 62.61                       | -1.90  | 0.329                | -1.764                         | -0.467          | -0.132                          | 1219.8                 |
| 394               | ACATCCAGTACTGTTACTGGA  | 538        | 62.71                       | -2.30  | 0.344                | -2.112                         | -0.590          | -0.343                          | 1675.2                 |
| 395               | CATCCAGTACTGTTACTGAT   | 539        | 62.12                       | -2.30  | 0.258                | -2.112                         | -0.643          | -0.504                          | 1414.0                 |
| 396               | ATCCAGTACTGTTACTGATTT  | 540        | 61.21                       | -2.30  | 0.124                | -2.112                         | -0.726          | -0.500                          | 1710.7                 |
| 397               | TCCAGTACTGTTACTGATTT   | 541        | 61.58                       | -2.30  | 0.178                | -2.112                         | -0.692          | -0.243                          | 2280.7                 |
| 398               | CCAGTACTGTTACTGATTTT   | 542        | 60.48                       | -2.30  | 0.017                | -2.112                         | -0.792          | -0.650                          | 2847.7                 |
| 399               | CAGTACTGTTACTGATTTT    | 543        | 56.84                       | -1.90  | -0.518               | -1.764                         | -0.992          | -0.635                          | 2830.2                 |
| 400               | AGTACTGTTACTGATTTT     | 544        | 55.82                       | -0.30  | -0.666               | -0.373                         | -0.555          | -0.588                          | 4336.3                 |
| 401               | GTACTGTTACTGATTTTTC    | 545        | 57.04                       | 0.40   | -0.488               | 0.236                          | -0.213          | -0.548                          | 6581.1                 |
| 402               | TACTGTTACTGATTTTTC     | 546        | 55.95                       | -0.10  | -0.649               | -0.199                         | -0.478          | -0.516                          | 5406.6                 |
| 403               | ACTGTTACTGATTTTTC      | 547        | 56.89                       | -0.10  | -0.510               | -0.199                         | -0.392          | -0.450                          | 6083.1                 |
| 404               | CTGTTACTGATTTTTC       | 548        | 56.67                       | -0.10  | -0.542               | -0.199                         | -0.412          | -0.482                          | 6585.7                 |

Table 4

| p5 Probe Position | DNA Probe Sequence | SEQ ID NO: | RNA/DNA T <sub>m</sub> (°C) | $\Delta G_{\text{fold}}$ (kcal/mole @ 35 °C) | T <sub>m</sub> Score | $\Delta G_{\text{fold}}$ Score | Composite Score | Window-Averaged Composite Score | HIV PRT GeneChip™ Data |
|-------------------|--------------------|------------|-----------------------------|--|----------------------|--------------------------------|-----------------|---------------------------------|------------------------|
| 405               | TGTTACTGATTTTCTTTT | 549        | 54.96                       | -0.10  | -0.793               | -0.199                         | -0.567          | -0.575                          | 3923.2                 |
| 406               | GTTACTGATTTTCTTTT  | 550        | 55.36                       | -0.10  | -0.734               | -0.199                         | -0.531          | -0.646                          | 4093.5                 |
| 407               | TACTGATTTTCTTTT    | 551        | 52.62                       | -0.10  | -1.136               | -0.199                         | -0.780          | -0.730                          | 1381.5                 |
| 408               | TACTGATTTTCTTTT    | 552        | 51.70                       | -0.10  | -1.272               | -0.199                         | -0.864          | -0.784                          | 1194.3                 |
| 409               | ACTGATTTTCTTTT     | 553        | 50.45                       | -0.10  | -1.454               | -0.199                         | -0.977          | -0.746                          | 2371.3                 |
| 410               | CTGATTTTCTTTT      | 554        | 50.45                       | -0.10  | -1.454               | -0.199                         | -0.977          | -0.682                          | 395.9                  |
| 411               | TGATTTTCTTTT       | 555        | 52.50                       | -0.10  | -1.155               | -0.199                         | -0.792          | -0.583                          | 230.7                  |
| 412               | GATTTTCTTTT        | 556        | 56.43                       | -0.10  | -0.578               | -0.149                         | -0.302          | -0.423                          | 314.9                  |
| 413               | ATTTTCTTTT         | 557        | 57.05                       | 0.80   | -0.487               | 0.583                          | -0.080          | -0.246                          | 276.1                  |
| 414               | TTTTCTTTT          | 558        | 56.99                       | 0.80   | -0.495               | 0.583                          | -0.085          | -0.046                          | 273.3                  |
| 415               | TTTTCTTTT          | 559        | 60.68                       | 0.80   | 0.045                | 0.583                          | 0.250           | 0.093                           | 628.4                  |
| 416               | TTTTCTTTT          | 560        | 60.85                       | 0.80   | 0.071                | 0.583                          | 0.265           | 0.156                           | 4661.4                 |
| 417               | TTTCTTTT           | 561        | 62.93                       | 0.70   | 0.377                | 0.496                          | 0.422           | 0.162                           | 411.2                  |
| 418               | TTCTTTT            | 562        | 65.01                       | -0.60  | 0.681                | -0.634                         | 0.181           | 0.166                           | 289.5                  |
| 419               | TTCTTTT            | 563        | 65.91                       | -1.00  | 0.813                | -0.982                         | 0.131           | 0.140                           | 244.8                  |
| 420               | TTTTT              | 564        | 64.52                       | -1.00  | 0.610                | -0.982                         | 0.005           | 0.096                           | 250.7                  |
| 421               | TTTTT              | 565        | 62.66                       | -1.00  | 0.337                | -0.982                         | -0.164          | 0.062                           | 207.8                  |
| 422               | TTTTT              | 566        | 65.23                       | -1.00  | 0.713                | -0.982                         | 0.069           | 0.106                           | 255.8                  |
| 423               | TTTTT              | 567        | 64.80                       | -1.00  | 0.651                | -0.982                         | 0.030           | 0.142                           | 356.8                  |
| 424               | TTTAACTT           | 568        | 66.83                       | -1.00  | 0.949                | -0.982                         | 0.215           | 0.204                           | 497.8                  |
| 425               | TTAACTT            | 569        | 69.50                       | -1.00  | 1.339                | -0.982                         | 0.457           | 0.348                           | 754.3                  |
| 426               | TAACTT             | 570        | 68.63                       | -1.00  | 1.212                | -0.982                         | 0.378           | 0.434                           | 902.4                  |
| 427               | AACTT              | 571        | 69.14                       | -1.00  | 1.286                | -0.982                         | 0.424           | 0.556                           | 1186.6                 |
| 428               | ACTT               | 572        | 71.66                       | -1.00  | 1.657                | -0.982                         | 0.654           | 0.505                           | 1514.9                 |
| 429               | CGTGGGATG          | 573        | 72.66                       | -0.60  | 1.804                | -0.634                         | 0.878           | 0.589                           | 2407.6                 |
| 430               | CTGGGATG           | 574        | 72.66                       | -0.60  | 1.804                | -0.634                         | 0.878           | 0.526                           | 3010.4                 |
| 431               | CTGGGATG           | 575        | 71.02                       | -1.30  | 1.563                | -1.243                         | 0.497           | 0.426                           | 3275.3                 |

Table 4

| p5 Probe Position | DNA Probe Sequence  | SEQ ID NO: | RNA/DNA T <sub>m</sub> (°C) | $\Delta G_{\text{fold}}$ (kcal/mole @ 35 °C) | T <sub>m</sub> Score | $\Delta G_{\text{fold}}$ Score | Composite Score | Window-Averaged Composite Score | HIV PRT GeneChip™ Data |
|-------------------|---------------------|------------|-----------------------------|--|----------------------|--------------------------------|-----------------|---------------------------------|------------------------|
| 432               | TCGGGATGGTATTCCTA   | 576        | 68.54                       | -1.30  | 1.199                | -1.243                         | 0.271           | 0.291                           | 2830.8                 |
| 433               | CGCGGATGGTATTCCTAA  | 577        | 66.48                       | -1.30  | 0.896                | -1.243                         | 0.083           | 0.108                           | 2620.5                 |
| 434               | CGGATGGTATTCCTAAT   | 578        | 62.46                       | -1.30  | 0.307                | -1.243                         | -0.282          | -0.058                          | 1827.8                 |
| 435               | GGGATGGTATTCCTAATT  | 579        | 62.37                       | -1.30  | 0.294                | -1.243                         | -0.290          | -0.244                          | 1957.4                 |
| 436               | GGGATGGTATTCCTAATG  | 580        | 59.71                       | -0.90  | -0.097               | -0.895                         | -0.400          | -0.330                          | 1686.2                 |
| 437               | GATGGTATTCCTAATGGA  | 581        | 58.45                       | -0.20  | -0.281               | -0.286                         | -0.283          | -0.306                          | 1395.0                 |
| 438               | ATGUGTATTCCTAATTGAA | 582        | 55.24                       | -0.20  | -0.752               | -0.286                         | -0.575          | -0.444                          | 1245.7                 |
| 439               | TGCTGATTCCTAATTGAC  | 583        | 55.76                       | -0.30  | -0.675               | -0.373                         | -0.561          | -0.473                          | 1314.0                 |
| 440               | GTGGTATTCCTAATTGAAT | 584        | 57.73                       | -0.30  | -0.387               | -0.373                         | -0.382          | -0.470                          | 1818.7                 |
| 441               | TGGTATTCCTAATTGAAT  | 585        | 55.15                       | -0.30  | -0.765               | -0.373                         | -0.616          | -0.474                          | 880.3                  |
| 442               | GGTATTCCTAATTGAATTC | 586        | 56.47                       | -0.30  | -0.572               | -0.373                         | -0.496          | -0.413                          | 1419.0                 |
| 443               | GTATTCCTAATTGAATTC  | 587        | 57.76                       | -0.30  | -0.383               | -0.373                         | -0.379          | -0.343                          | 1567.9                 |
| 444               | TATTCCTAATTGAATTC   | 588        | 58.57                       | -0.30  | -0.264               | -0.373                         | -0.306          | -0.248                          | 1959.4                 |
| 445               | TATTCCTAATTGAATTC   | 589        | 60.26                       | -0.30  | -0.016               | -0.373                         | -0.152          | -0.161                          | 2971.8                 |
| 446               | TTCCTAATTGAATTC     | 590        | 60.45                       | -0.10  | 0.013                | -0.199                         | -0.068          | -0.200                          | 1898.5                 |
| 447               | TCTAATTGAATTC       | 591        | 61.36                       | 0.70   | 0.146                | 0.496                          | 0.279           | -0.300                          | 1392.3                 |
| 448               | TCTAATTGAATTC       | 592        | 58.27                       | 0.70   | -0.308               | 0.496                          | -0.002          | -0.382                          | 1143.2                 |
| 449               | CTAATTGAATTC        | 593        | 54.92                       | -0.70  | -0.800               | -0.721                         | -0.770          | -0.467                          | 427.7                  |
| 450               | TAATTGAATTC         | 594        | 55.84                       | -1.90  | -0.684               | -1.764                         | -1.082          | -0.545                          | 148.5                  |
| 451               | TAATTGAATTC         | 595        | 57.61                       | -2.10  | -0.404               | -1.938                         | -0.987          | -0.677                          | 259.1                  |
| 452               | ATTGAATTC           | 596        | 61.42                       | -2.10  | 0.154                | -1.938                         | -0.641          | -0.751                          | 241.9                  |
| 453               | TGGAATTC            | 597        | 61.76                       | -2.10  | 0.205                | -1.938                         | -0.609          | -0.730                          | 808.1                  |
| 454               | TGAATTC             | 598        | 61.34                       | -2.10  | 0.143                | -1.938                         | -0.648          | -0.586                          | 351.6                  |
| 455               | GAACTTC             | 599        | 62.71                       | -2.10  | 0.344                | -1.938                         | -0.523          | -0.445                          | 498.7                  |
| 456               | AACTTC              | 600        | 61.63                       | -2.10  | 0.186                | -1.938                         | -0.621          | -0.262                          | 407.4                  |
| 457               | ACTTC               | 601        | 66.97                       | -1.90  | 0.969                | -1.764                         | -0.069          | -0.138                          | 492.1                  |
| 458               | CTTC                | 602        | 66.75                       | -1.00  | 0.937                | -0.982                         | 0.208           | -0.049                          | 736.1                  |

Table 4

| p5 Probe Position | DNA Probe Sequence  | SEQ ID NO: | RNA/DNA T <sub>m</sub> (°C) | $\Delta G_{fold}$ (kcal/mole @ 35 °C) | T <sub>m</sub> Score | $\Delta G_{fold}$ Score | Composite Score | Window-Averaged Composite Score | HIV PRT GeneChip™ Data |
|-------------------|---------------------|------------|-----------------------------|---------------------------------------|----------------------|-------------------------|-----------------|---------------------------------|------------------------|
| 459               | TTCCAGAGGCTCTGAGTTC | 603        | 66.31                       | -0.20                                 | 0.872                | -0.266                  | 0.432           | 0.058                           | 815.2                  |
| 460               | TCCAGAGGCTCTGAGTTC  | 604        | 67.98                       | -1.20                                 | 1.116                | -1.156                  | 0.253           | 0.101                           | 888.8                  |
| 461               | CCAGAGGCTCTGAGTTC   | 605        | 67.98                       | -1.40                                 | 1.116                | -1.330                  | 0.187           | 0.049                           | 2021.6                 |
| 462               | CCAGAGGCTCTGAGTTC   | 606        | 66.10                       | -1.40                                 | 0.842                | -1.330                  | 0.017           | 0.043                           | 1988.5                 |
| 463               | CAGAGGCTCTGAGTTC    | 607        | 62.41                       | -1.40                                 | 0.300                | -1.330                  | -0.319          | 0.082                           | 2008.8                 |
| 464               | AGAGGCTCTGAGTTC     | 608        | 60.43                       | -1.20                                 | 0.009                | -1.156                  | -0.434          | 0.105                           | 2631.8                 |
| 465               | GAGGCTCTGAGTTC      | 609        | 60.20                       | -0.50                                 | -0.025               | -0.547                  | -0.223          | 0.151                           | 3052.8                 |
| 466               | AGGCTCTGAGTTC       | 610        | 59.12                       | 0.30                                  | -0.183               | 0.149                   | -0.057          | 0.242                           | 3509.3                 |
| 467               | AGCTCTGAGTTC        | 611        | 60.75                       | 0.30                                  | 0.066                | 0.149                   | 0.091           | 0.214                           | 3221.6                 |
| 468               | GCTCTGAGTTC         | 612        | 58.29                       | 0.30                                  | -0.305               | 0.149                   | -0.132          | 0.246                           | 3677.1                 |
| 469               | TCTGAGTTC           | 613        | 55.25                       | 0.30                                  | -0.751               | 0.149                   | -0.409          | 0.238                           | 1176.8                 |
| 470               | CTGAGTTC            | 614        | 57.04                       | 0.10                                  | -0.488               | -0.025                  | -0.312          | 0.265                           | 1188.1                 |
| 471               | TGAGTTC             | 615        | 55.29                       | 0.10                                  | -0.745               | -0.025                  | -0.471          | 0.262                           | 666.3                  |
| 472               | TGAGTTC             | 616        | 56.35                       | 0.10                                  | -0.589               | -0.025                  | -0.375          | 0.224                           | 674.0                  |
| 473               | GAGTTC              | 617        | 58.57                       | 0.10                                  | -0.263               | -0.025                  | -0.173          | 0.256                           | 1471.4                 |
| 474               | AGTTC               | 618        | 58.61                       | 0.10                                  | -0.257               | -0.025                  | -0.169          | 0.240                           | 1493.5                 |
| 475               | GTCTCTTAAGTTC       | 619        | 60.59                       | 0.10                                  | 0.032                | -0.025                  | 0.011           | 0.247                           | 2191.5                 |
| 476               | TCTCTTAAGTTC        | 620        | 57.16                       | 0.10                                  | -0.471               | -0.025                  | -0.301          | 0.347                           | 1410.3                 |
| 477               | TCTCTTAAGTTC        | 621        | 58.23                       | 0.10                                  | -0.314               | -0.025                  | -0.204          | 0.443                           | 1262.8                 |
| 478               | CTCTTAAGTTC         | 622        | 54.79                       | 0.10                                  | -0.817               | -0.025                  | -0.516          | 0.549                           | 1072.9                 |
| 479               | TCTTAAGTTC          | 623        | 50.95                       | 0.10                                  | -1.382               | -0.025                  | -0.866          | 0.629                           | 540.9                  |
| 480               | CTTAAGTTC           | 624        | 49.77                       | 0.50                                  | -1.554               | 0.323                   | -0.841          | 0.605                           | 539.2                  |
| 481               | TATAAGTTC           | 625        | 48.99                       | 0.50                                  | -1.688               | 0.323                   | -0.912          | 0.768                           | 709.0                  |
| 482               | TATAAGTTC           | 626        | 50.64                       | 0.50                                  | -1.427               | 0.323                   | -0.762          | 0.775                           | 978.1                  |
| 483               | ATAAGTTC            | 627        | 50.64                       | 0.50                                  | -1.427               | 0.323                   | -0.762          | 0.732                           | 1217.7                 |
| 484               | TAAAGTTC            | 628        | 51.15                       | 0.50                                  | -1.352               | 0.323                   | -0.716          | 0.603                           | 1748.1                 |
| 485               | TAAGTTC             | 629        | 52.79                       | 0.50                                  | -1.112               | 0.323                   | -0.567          | 0.646                           | 2511.5                 |

Table 4

| p5 Probe Position | DNA Probe Sequence    | SEQ ID NO: | RNA/DNA $T_m$ (°C) | $\Delta G_{\text{Mfold}}$ (kcal/mole @ 35 °C) | $T_m$ Score | $\Delta G_{\text{Mfold}}$ Score | Composite Score | Window-Averaged Composite Score | HIV PRT GeneChip™ Data |
|-------------------|-----------------------|------------|--------------------|---|-------------|---------------------------------|-----------------|---------------------------------|------------------------|
| 486               | AGGTCCTGGAATCTACTA    | 630        | 52.79              | 0.50  | -1.112      | 0.323                           | -0.567          | -0.643                          | 2897.2                 |
| 487               | AGTCTCTGAAATCTACTAA   | 631        | 52.79              | 0.50  | -1.112      | 0.323                           | -0.567          | -0.663                          | 2887.6                 |
| 488               | GTTCCTGGAATCTACTAAT   | 632        | 52.65              | 0.50  | -1.133      | 0.323                           | -0.580          | -0.726                          | 4421.3                 |
| 489               | TTCTGGAATCTACTAAAT    | 633        | 50.14              | 0.70  | -1.500      | 0.496                           | -0.741          | -0.832                          | 1937.7                 |
| 490               | TCTGGAATCTACTAAATTT   | 634        | 50.14              | 0.20  | -1.500      | 0.062                           | -0.906          | -0.962                          | 1773.3                 |
| 491               | CTCTGGAATCTACTAAATTT  | 635        | 49.31              | -0.30   | -1.622      | -0.373                          | -1.147          | -1.102                          | 1491.1                 |
| 492               | CTGGAATCTACTAAATTTTC  | 636        | 48.55              | -0.80   | -1.734      | -0.634                          | -1.316          | -1.171                          | 376.6                  |
| 493               | CTGAAATCTACTAAATTTCT  | 637        | 49.31              | -1.30   | -1.622      | -1.243                          | -1.478          | -1.178                          | 371.9                  |
| 494               | TGAAATCTACTAAATTTCTC  | 638        | 48.55              | -1.30   | -1.734      | -1.243                          | -1.547          | -1.092                          | 415.2                  |
| 495               | GAAATCTACTAAATTTCTCC  | 639        | 52.45              | -0.90   | -1.161      | -0.895                          | -1.060          | -0.938                          | 1097.9                 |
| 496               | AAATCTACTAAATTTCTCCA  | 640        | 52.47              | -0.10   | -1.158      | -0.199                          | -0.794          | -0.778                          | 1429.1                 |
| 497               | AACTCTACTAAATTTCTCCAT | 641        | 54.25              | 0.90  | -0.897      | 0.670                           | -0.301          | -0.620                          | 1812.5                 |
| 498               | ATCTACTAAATTTCTCCATTT | 642        | 56.46              | 1.00  | -0.572      | 0.757                           | -0.067          | -0.465                          | 1843.4                 |
| 499               | TCTACTAAATTTCTCCATTTA | 643        | 56.80              | 0.50  | -0.523      | 0.323                           | -0.202          | -0.424                          | 1506.1                 |
| 500               | CTACTAAATTTCTCCATTTA  | 644        | 54.93              | 0.50  | -0.797      | 0.323                           | -0.372          | -0.326                          | 1694.7                 |
| 501               | TACTAAATTTCTCCATTTAG  | 645        | 53.14              | 0.30  | -1.060      | 0.149                           | -0.600          | -0.366                          | 946.7                  |
| 502               | ACTAAATTTCTCCATTTAGT  | 646        | 56.69              | -0.70   | -0.539      | -0.721                          | -0.608          | -0.402                          | 1114.3                 |
| 503               | CTAATTTCTCCATTTAGTA   | 647        | 55.57              | 0.00  | -0.704      | -0.112                          | -0.479          | -0.360                          | 963.9                  |
| 504               | TAAATTTCTCCATTTAGTAC  | 648        | 54.12              | 0.80  | -0.917      | 0.323                           | -0.446          | -0.274                          | 1347.9                 |
| 505               | AAATTTCTCCATTTAGTACT  | 649        | 56.69              | 0.70  | -0.539      | 0.496                           | -0.145          | -0.130                          | 2067.7                 |
| 506               | ATTTCTCCATTTAGTACTG   | 650        | 58.66              | 0.80  | -0.250      | 0.583                           | 0.067           | 0.032                           | 2724.2                 |
| 507               | TTTCTCCATTTAGTACTGT   | 651        | 61.92              | 0.80  | 0.228       | 0.410                           | 0.297           | 0.186                           | 3367.9                 |
| 508               | TTTCTCCATTTAGTACTGTC  | 652        | 63.10              | 0.80  | 0.401       | 0.410                           | 0.404           | 0.314                           | 5235.8                 |
| 509               | TTCTCCATTTAGTACTGCT   | 653        | 64.84              | 0.60  | 0.656       | 0.410                           | 0.562           | 0.372                           | 6423.5                 |
| 510               | TCTCCATTTAGTACTGCTT   | 654        | 64.84              | 0.80  | 0.656       | 0.410                           | 0.562           | 0.366                           | 7759.9                 |
| 511               | CTCCATTTAGTACTGCTTT   | 655        | 63.63              | 0.80  | 0.479       | 0.410                           | 0.453           | 0.342                           | 8001.5                 |
| 512               | TCCATTTAGTACTGCTTTT   | 656        | 61.92              | 0.60  | 0.228       | 0.410                           | 0.297           | 0.273                           | 5512.4                 |

Table 4

| p5 Probe Position | DNA Probe Sequence | SEQ ID NO. | RNA/DNA $T_m$ (°C) | $\Delta G_{fold}$ (kcal/mole @ 35 °C) | $T_m$ Score | $\Delta G_{fold}$ Score | Composite Score | Window-Averaged Composite Score | HIV PRT GeneChip™ Data |
|-------------------|--------------------|------------|--------------------|---------------------------------------|-------------|-------------------------|-----------------|---------------------------------|------------------------|
| 513               | CCATTAGTACTGCTTTT  | 657        | 60.78              | 0.80                                  | 0.061       | 0.410                   | 0.194           | 0.240                           | 5300.0                 |
| 514               | CATTAGTACTGCTTTT   | 658        | 57.04              | 0.80                                  | -0.489      | 0.583                   | -0.081          | 0.442                           | 3902.1                 |
| 515               | ATTAGTACTGCTTTT    | 659        | 57.08              | 0.80                                  | -0.482      | 0.583                   | -0.077          | 0.000                           | 4841.8                 |
| 516               | TTAGTACTGCTTTT     | 660        | 59.26              | 0.80                                  | -0.162      | 0.583                   | 0.121           | 0.084                           | 4888.4                 |
| 517               | TAGTACTGCTTTT      | 661        | 59.26              | 0.80                                  | -0.162      | 0.583                   | 0.121           | 0.160                           | 5477.3                 |
| 518               | TAGTACTGCTTTT      | 662        | 59.26              | 0.80                                  | -0.162      | 0.583                   | 0.121           | 0.242                           | 5064.9                 |
| 519               | AGTACTGCTTTT       | 663        | 59.26              | 1.00                                  | -0.162      | 0.757                   | 0.187           | 0.340                           | 5580.3                 |
| 520               | GACTGCTTTT         | 664        | 59.04              | 2.70                                  | -0.195      | 2.236                   | 0.729           | 0.400                           | 5478.3                 |
| 521               | TACTGCTTTT         | 665        | 55.71              | 2.90                                  | -0.683      | 2.410                   | 0.492           | 0.480                           | 2275.5                 |
| 522               | ACTGCTTTT          | 666        | 59.07              | 1.70                                  | -0.190      | 1.366                   | 0.402           | 0.524                           | 1730.8                 |
| 523               | CTGCTTTT           | 667        | 62.92              | 1.70                                  | 0.374       | 1.366                   | 0.751           | 0.449                           | 2405.5                 |
| 524               | TGCTTTT            | 668        | 62.14              | 1.70                                  | 0.260       | 1.366                   | 0.680           | 0.258                           | 1942.0                 |
| 525               | GTCTTTT            | 669        | 60.05              | 1.50                                  | -0.047      | 1.192                   | 0.424           | 0.068                           | 2085.6                 |
| 526               | CTTTT              | 670        | 54.99              | 0.60                                  | -0.788      | 0.410                   | -0.333          | -0.106                          | 493.2                  |
| 527               | TTTTT              | 671        | 53.75              | 0.10                                  | -0.971      | -0.025                  | -0.612          | -0.309                          | 532.7                  |
| 528               | TTTTT              | 672        | 51.30              | 0.10                                  | -1.331      | -0.025                  | -0.835          | -0.602                          | 280.0                  |
| 529               | TTTTT              | 673        | 51.49              | 0.10                                  | -1.302      | -0.025                  | -0.817          | -0.640                          | 440.8                  |
| 530               | TTTTT              | 674        | 53.08              | 0.10                                  | -1.069      | -0.025                  | -0.672          | -0.652                          | 463.1                  |
| 531               | TTTTT              | 675        | 52.74              | 0.10                                  | -1.119      | -0.025                  | -0.704          | -0.639                          | 579.0                  |
| 532               | TTTTT              | 676        | 54.90              | 0.10                                  | -0.802      | -0.025                  | -0.507          | -0.572                          | 673.7                  |
| 533               | TTTTT              | 677        | 55.85              | 0.10                                  | -0.663      | -0.025                  | -0.421          | -0.504                          | 837.0                  |
| 534               | TTTTT              | 678        | 54.78              | 0.10                                  | -0.820      | -0.025                  | -0.518          | -0.490                          | 1061.9                 |
| 535               | TTTTT              | 679        | 55.14              | 0.30                                  | -0.679      | 0.149                   | -0.365          | -0.502                          | 855.0                  |
| 536               | TTTTT              | 680        | 54.87              | 0.60                                  | -0.806      | 0.410                   | -0.344          | -0.562                          | 775.0                  |
| 537               | TTTTT              | 681        | 54.56              | 0.00                                  | -0.862      | -0.112                  | -0.571          | -0.584                          | 773.6                  |
| 538               | TTTTT              | 682        | 55.42              | -1.00                                 | -0.726      | -0.982                  | -0.823          | -0.642                          | 702.5                  |
| 539               | TTTTT              | 683        | 55.37              | -1.20                                 | -0.733      | -1.156                  | -0.853          | -0.775                          | 387.5                  |

Table 4

| p5 Probe Position | DNA Probe Sequence    | SEQ ID NO: | RNA/DNA $T_m$ (°C) | $\Delta G_{\text{fold}}$ (kcal/mole @ 35 °C) | $T_m$ Score | $\Delta G_{\text{fold}}$ Score | Composite Score | Window-Averaged Composite Score | HIV PRT GeneChip™ Data |
|-------------------|-----------------------|------------|--------------------|--|-------------|--------------------------------|-----------------|---------------------------------|------------------------|
| 540               | GCACAACTACGGAGTATGTT  | 684        | 58.33              | -1.20  | -0.298      | -1.156                         | -0.624          | -0.924                          | 435.3                  |
| 541               | GCACAACTACGGAGTATGTTA | 685        | 55.24              | -1.20  | -0.753      | -1.156                         | -0.906          | -0.974                          | 93.7                   |
| 542               | CAAAATACGAGTATGTTAT   | 686        | 51.30              | -1.20  | -1.331      | -1.156                         | -1.264          | -0.973                          | 50.0                   |
| 543               | AAATACGAGTATGTTATG    | 687        | 49.96              | -1.20  | -1.527      | -1.156                         | -1.386          | -0.809                          | 50.4                   |
| 544               | AATACGAGTATGTTATGG    | 688        | 54.30              | -1.00  | -0.890      | -0.982                         | -0.925          | -0.688                          | 64.7                   |
| 545               | ATACTGAGTATGTTATGGA   | 689        | 57.60              | -0.30  | -0.408      | -0.373                         | -0.394          | -0.483                          | 76.0                   |
| 546               | TACTGGAGTATGTTATGGAT  | 690        | 57.60              | 0.40   | -0.406      | 0.236                          | -0.162          | -0.236                          | 86.0                   |
| 547               | ACTGGAGTATGTTATGGATT  | 691        | 58.53              | 1.30   | -0.269      | 1.018                          | 0.220           | -0.009                          | 123.4                  |
| 548               | CTGGAGTATGTTATGGATTC  | 692        | 59.39              | 2.00   | -0.144      | 1.627                          | 0.529           | 0.436                           | 121.5                  |
| 549               | TGGAGTATGTTATGGATTC   | 693        | 59.39              | 1.80   | -0.144      | 1.453                          | 0.463           | 0.210                           | 647.3                  |
| 550               | GGAGTATGTTATGGATTC    | 694        | 60.95              | 0.60   | 0.086       | 0.410                          | 0.209           | 0.286                           | 161.5                  |
| 551               | GAGTATGTTATGGATTC     | 695        | 59.52              | 0.60   | -0.124      | 0.410                          | 0.079           | 0.321                           | 129.9                  |
| 552               | AGTATGTTATGGATTC      | 696        | 58.31              | 1.10   | 0.074       | 0.844                          | 0.367           | 0.463                           | 112.5                  |
| 553               | GTATGTTATGGATTC       | 697        | 60.87              | 1.10   | 0.074       | 0.844                          | 0.367           | 0.463                           | 112.5                  |
| 554               | TATGTTATGGATTC        | 698        | 61.97              | 1.10   | 0.236       | 0.844                          | 0.467           | 0.575                           | 134.6                  |
| 555               | ATTGTTATGGATTC        | 699        | 66.52              | 1.10   | 0.902       | 0.844                          | 0.880           | 0.669                           | 191.6                  |
| 556               | TGTTATGGATTC          | 700        | 70.34              | 0.70   | 1.463       | 0.496                          | 1.096           | 0.714                           | 254.5                  |
| 557               | TGTTATGGATTC          | 701        | 71.11              | 0.20   | 1.577       | 0.062                          | 1.001           | 0.748                           | 332.2                  |
| 558               | GTATGGATTC            | 702        | 68.95              | 0.00   | 1.259       | -0.112                         | 0.738           | 0.761                           | 285.0                  |
| 559               | TATGGATTC             | 703        | 65.78              | 0.00   | 0.795       | -0.112                         | 0.450           | 0.724                           | 285.0                  |
| 560               | GATTC                 | 704        | 66.68              | 0.00   | 0.925       | -0.112                         | 0.531           | 0.737                           | 464.0                  |
| 561               | TGATTC                | 705        | 67.04              | 0.20   | 0.979       | 0.062                          | 0.630           | 0.663                           | 492.5                  |
| 562               | GATTC                 | 706        | 67.51              | 1.10   | 1.048       | 0.844                          | 0.970           | 0.624                           | 639.7                  |
| 563               | ATTC                  | 707        | 65.34              | 1.30   | 0.729       | 1.018                          | 0.839           | 0.605                           | 512.4                  |
| 564               | ATTC                  | 708        | 63.94              | 0.60   | 0.524       | 0.410                          | 0.481           | 0.513                           | 393.4                  |
| 565               | TTC                   | 709        | 65.24              | 0.20   | 0.716       | 0.062                          | 0.467           | 0.364                           | 334.3                  |
| 566               | TTC                   | 710        | 62.85              | 0.20   | 0.364       | 0.062                          | 0.249           | 0.481                           | 308.2                  |

Table 4

| p5 Probe Position | DNA Probe Sequence     | SEQ ID NO: | RNA/DNA T <sub>m</sub> (°C) | $\Delta G_{fold}$ (kcal/mole @ 35 °C) | T <sub>m</sub> Score | $\Delta G_{fold}$ Score | Composite Score | Window-Averaged Composite Score | HIV PRT GeneChip™ Data |
|-------------------|------------------------|------------|-----------------------------|---------------------------------------|----------------------|-------------------------|-----------------|---------------------------------|------------------------|
| 567               | CTCAGGCCCAATTTTGAAA    | 711        | 59.62                       | 0.20                                  | -0.109               | 0.062                   | -0.044          | -0.048                          | 199.2                  |
| 568               | TCAGGCCCAATTTTGAAAT    | 712        | 57.85                       | 0.20                                  | -0.369               | 0.062                   | -0.205          | -0.223                          | 164.3                  |
| 569               | CAGGCCCAATTTTGAAAT     | 713        | 56.95                       | -0.50                                 | -0.501               | -0.547                  | -0.518          | -0.412                          | 125.6                  |
| 570               | AGGCCCAATTTTGAAATTT    | 714        | 56.09                       | -1.00                                 | -0.627               | -0.982                  | -0.762          | -0.524                          | 102.6                  |
| 571               | GCCCAATTTTGAAATTTT     | 715        | 56.23                       | -1.00                                 | -0.606               | -0.982                  | -0.749          | -0.688                          | 91.6                   |
| 572               | GCCCAATTTTGAAATTTTC    | 716        | 55.07                       | -1.00                                 | -0.777               | -0.982                  | -0.855          | -0.806                          | 76.2                   |
| 573               | CCCAATTTTGAAATTTTCC    | 717        | 54.96                       | -1.00                                 | -0.792               | -0.982                  | -0.864          | -0.887                          | 78.3                   |
| 574               | CAATTTTGAAATTTTCCCT    | 718        | 54.96                       | -1.00                                 | -0.792               | -0.982                  | -0.864          | -0.841                          | 84.8                   |
| 575               | CAATTTTGAAATTTTCCCT    | 719        | 53.17                       | -1.00                                 | -1.065               | -0.982                  | -1.027          | -0.755                          | 162.0                  |
| 576               | AAATTTTGAAATTTTCCCT    | 720        | 52.25                       | -0.80                                 | -1.190               | -0.808                  | -1.045          | -0.634                          | 539.5                  |
| 577               | TTTTTGAAATTTTCCCTTC    | 721        | 55.17                       | 0.10                                  | -0.762               | -0.025                  | -0.482          | -0.514                          | 1787.3                 |
| 578               | TTTTTGAAATTTTCCCTTC    | 722        | 58.88                       | 0.10                                  | -0.219               | -0.025                  | -0.145          | -0.389                          | 6354.2                 |
| 579               | TTTGAAATTTTCCCTTCCT    | 723        | 60.39                       | 0.10                                  | 0.004                | -0.025                  | -0.007          | -0.243                          | 9513.6                 |
| 580               | TTTGAAATTTTCCCTTCCT    | 724        | 60.39                       | 0.10                                  | 0.004                | -0.025                  | -0.007          | -0.062                          | 10680.0                |
| 581               | TTTGAAATTTTCCCTTCCTTT  | 725        | 60.39                       | 0.10                                  | 0.004                | -0.025                  | -0.007          | -0.102                          | 11202.0                |
| 582               | TGAAATTTTCCCTTCCTTTT   | 726        | 60.39                       | 0.10                                  | 0.004                | -0.025                  | -0.007          | -0.293                          | 11543.0                |
| 583               | GAATTTTCCCTTCCTTCCTTC  | 727        | 61.81                       | 0.40                                  | 0.212                | 0.236                   | 0.221           | 0.506                           | 14774.0                |
| 584               | AAATTTTCCCTTCCTTTTCCA  | 728        | 64.17                       | 1.20                                  | 0.557                | 0.931                   | 0.699           | 0.952                           | 18197.0                |
| 585               | AAATTTTCCCTTCCTTTTCCA  | 729        | 67.39                       | 1.70                                  | 1.030                | 1.366                   | 1.158           | 1.307                           | 21410.0                |
| 586               | ATTTTCCCTTCCTTTTCCATT  | 730        | 69.58                       | 4.00                                  | 1.351                | 3.366                   | 2.117           | 1.679                           | 22869.0                |
| 587               | TTTTCCCTTCCTTTTCCATT   | 731        | 69.96                       | 5.00                                  | 1.408                | 4.236                   | 2.482           | 2.039                           | 21818.0                |
| 588               | TTTCCCTTCCTTTTCCATT    | 732        | 69.96                       | 5.00                                  | 1.408                | 4.236                   | 2.482           | 2.113                           | 21341.0                |
| 589               | TTCCCTTCCTTTTCCATTTC   | 733        | 71.19                       | 5.00                                  | 1.588                | 4.236                   | 2.594           | 2.085                           | 22063.0                |
| 590               | TCCTTCCTTTTCCATTTCCT   | 734        | 72.77                       | 5.00                                  | 1.820                | 4.236                   | 2.738           | 1.863                           | 22152.0                |
| 591               | CCCTTCCTTTTCCATTTCG    | 735        | 71.01                       | 0.90                                  | 1.561                | 0.670                   | 1.223           | 1.571                           | 20764.0                |
| 592               | CTTCCTTCCTTTTCCATTTCG  | 736        | 70.68                       | 0.20                                  | 1.513                | 0.062                   | 0.961           | 1.289                           | 12579.0                |
| 593               | CTTCCTTCCTTTTCCATTTCGA | 737        | 66.30                       | 0.20                                  | 0.870                | 0.062                   | 0.563           | 0.945                           | 9036.3                 |

Table 4

| p5 Probe Position | DNA Probe Sequence    | SEQ ID NO: | RNA/DNA T <sub>m</sub> (°C) | $\Delta G_{\text{fold}}$ (kcal/mole @ 35 °C) | T <sub>m</sub> Score | $\Delta G_{\text{fold}}$ Score | Composite Score | Window-Averaged Composite Score | HIV PRT GeneChip™ Data |
|-------------------|-----------------------|------------|-----------------------------|--|----------------------|--------------------------------|-----------------|---------------------------------|------------------------|
| 584               | TTCTCTTTCCATTTCTGTAC  | 738        | 64.87                       | 0.20   | 0.660                | 0.062                          | 0.433           | 0.505                           | 8251.8                 |
| 595               | TCCTTTTCCTTTCTGTAGA   | 739        | 65.74                       | 0.20   | 0.788                | 0.062                          | 0.512           | 0.267                           | 20788.0                |
| 596               | CCCTTTTCCTTTCTGTACAA  | 740        | 62.11                       | 0.20   | 0.256                | 0.062                          | 0.182           | 0.024                           | 7073.9                 |
| 597               | CTTTTCCTTTCTGTACAAA   | 741        | 56.39                       | 0.20   | -0.583               | 0.062                          | -0.338          | -0.163                          | 2832.4                 |
| 598               | TTTTCCTTTCTGTACAAAT   | 742        | 54.49                       | 0.20   | -0.862               | 0.062                          | -0.511          | -0.300                          | 1897.3                 |
| 599               | TTTTCCTTTCTGTACAAAT   | 743        | 54.49                       | -0.30  | -0.862               | -0.373                         | -0.676          | -0.449                          | 2158.1                 |
| 600               | TTTTCCTTTCTGTACAAAT   | 744        | 54.49                       | -0.30  | -0.862               | -0.373                         | -0.676          | -0.608                          | 2215.9                 |
| 601               | TTTTCCTTTCTGTACAAAT   | 745        | 55.43                       | -0.30  | -0.724               | -0.373                         | -0.591          | -0.695                          | 2168.6                 |
| 602               | CAATTTCTGTACAAATTTCT  | 746        | 56.07                       | -0.30  | -0.631               | -0.373                         | -0.533          | -0.708                          | 2025.8                 |
| 603               | CAATTTCTGTACAAATTTCTA | 747        | 51.65                       | -0.30  | -1.278               | -0.373                         | -0.934          | -0.708                          | 1277.2                 |
| 604               | ATTTCTGTACAAATTTCTAC  | 748        | 50.83                       | -0.10  | -1.398               | -0.199                         | -0.943          | -0.736                          | 1944.8                 |
| 605               | TTTCTGTACAAATTTCTACT  | 749        | 52.78                       | 0.40   | -1.112               | 0.236                          | -0.600          | -0.790                          | 2504.3                 |
| 606               | TTCTGTACAAATTTCTACTA  | 750        | 51.90                       | 0.40   | -1.242               | 0.236                          | -0.681          | -0.876                          | 2941.5                 |
| 607               | CTGTACAAATTTCTACTAAT  | 751        | 49.84                       | 0.40   | -1.544               | 0.236                          | -0.868          | -0.846                          | 2694.8                 |
| 608               | CTGTACAAATTTCTACTAAT  | 752        | 48.73                       | 0.40   | -1.707               | 0.236                          | -0.969          | -0.827                          | 2610.7                 |
| 609               | CTGTACAAATTTCTACTAATG | 753        | 46.88                       | 0.40   | -1.979               | 0.236                          | -1.137          | -0.845                          | 1678.1                 |
| 610               | GTACAAATTTCTACTAATGC  | 754        | 50.66                       | 0.60   | -1.424               | 0.410                          | -0.727          | -0.854                          | 5877.3                 |
| 611               | TACAAATTTCTACTAATGCT  | 755        | 49.82                       | 0.60   | -1.547               | 0.410                          | -0.803          | -0.849                          | 4461.0                 |
| 612               | ACAAATTTCTACTAATGCTT  | 756        | 50.65                       | 0.60   | -1.425               | 0.410                          | -0.728          | -0.876                          | 5943.2                 |
| 613               | CAAAATTTCTACTAATGCTTT | 757        | 50.46                       | 0.60   | -1.453               | 0.410                          | -0.745          | -0.753                          | 6492.9                 |
| 614               | AAATTTCTACTAATGCTTTT  | 758        | 49.47                       | 0.60   | -1.599               | 0.410                          | -0.836          | -0.745                          | 6875.0                 |
| 615               | AAATTTCTACTAATGCTTTTA | 759        | 50.61                       | 0.60   | -1.431               | 0.410                          | -0.731          | -0.722                          | 7950.3                 |
| 616               | ATTTCTACTAATGCTTTTAT  | 760        | 52.40                       | 0.20   | -1.189               | 0.062                          | -0.701          | -0.720                          | 6885.8                 |
| 617               | TTTCTACTAATGCTTTTAT   | 761        | 52.72                       | 0.20   | -1.122               | 0.062                          | -0.672          | -0.749                          | 6443.2                 |
| 618               | TTTCTACTAATGCTTTTAT   | 762        | 52.72                       | 0.20   | -1.122               | 0.062                          | -0.672          | -0.731                          | 6331.0                 |
| 619               | TTCTACTAATGCTTTTATTT  | 763        | 52.72                       | 0.20   | -1.122               | 0.062                          | -0.672          | -0.748                          | 5952.5                 |
| 620               | CTACTAATGCTTTTATTTT   | 764        | 51.81                       | 0.20   | -1.255               | 0.062                          | -0.755          |                                 |                        |

Table 4

| p5 Probe Position | DNA Probe Sequence    | SEQ ID NO: | RNA/DNA T <sub>m</sub> (°C) | $\Delta G_{\text{fold}}$ (kcal/mole @ 35 °C) | T <sub>m</sub> Score | $\Delta G_{\text{fold}}$ Score | Composite Score | Window-Averaged Composite Score | HIV PRT GeneChip™ Data |
|-------------------|-----------------------|------------|-----------------------------|--|----------------------|--------------------------------|-----------------|---------------------------------|------------------------|
| 621               | TACTAATGCTTTTATTTTT   | 765        | 50.18                       | 0.20   | -1.494               | 0.062                          | -0.903          | -0.724                          | 2662.8                 |
| 622               | ACTAATGCTTTTATTTTT    | 766        | 51.96                       | 0.20   | -1.233               | 0.062                          | -0.741          | -0.667                          | 3034.0                 |
| 623               | CTAATGCTTTTATTTTTCT   | 767        | 53.41                       | 0.20   | -1.021               | 0.062                          | -0.609          | -0.543                          | 2198.5                 |
| 624               | TAAAGCTTTTATTTTTCTT   | 768        | 51.76                       | 0.40   | -1.263               | 0.236                          | -0.894          | -0.346                          | 1670.1                 |
| 625               | AATGCTTTTATTTTTCTTC   | 769        | 53.61                       | 1.10   | -0.992               | 0.844                          | -0.294          | -0.038                          | 3039.4                 |
| 626               | ATGCTTTTATTTTTCTTCT   | 770        | 57.66                       | 2.10   | -0.397               | 1.714                          | 0.405           | 0.423                           | 3873.8                 |
| 627               | TGCTTTTATTTTTCTTCG    | 771        | 57.60                       | 2.80   | -0.406               | 2.323                          | 0.631           | 0.463                           | 3609.7                 |
| 628               | GCCTTTTATTTTTCTTCTG   | 772        | 60.96                       | 3.10   | 0.087                | 2.583                          | 1.036           | 0.484                           | 4891.4                 |
| 629               | CTTTTATTTTTCTTCGTC    | 773        | 57.96                       | 3.10   | -0.363               | 2.583                          | 0.763           | 0.480                           | 3071.6                 |
| 630               | TTTATTTTTTCTTCGTC     | 774        | 57.22                       | 3.10   | -0.461               | 2.583                          | 0.696           | 0.304                           | 2667.2                 |
| 631               | TTATTTTTTCTTCGTC      | 775        | 54.81                       | 1.70   | -0.816               | 1.366                          | 0.013           | 0.342                           | 2293.1                 |
| 632               | TTATTTTTTCTTCGCAAT    | 776        | 54.46                       | 1.20   | -0.866               | 0.931                          | -0.183          | 0.232                           | 2123.0                 |
| 633               | TATTTTTTCTTCGCAATG    | 777        | 54.08                       | 1.20   | -0.922               | 0.931                          | -0.218          | 0.237                           | 1914.7                 |
| 634               | ATTTTCTTCGTCGAATG     | 778        | 57.36                       | 1.20   | -0.442               | 0.931                          | 0.080           | 0.263                           | 2174.1                 |
| 635               | TTTTTCTTCGTCGAATGC    | 779        | 61.67                       | 1.20   | 0.192                | 0.931                          | 0.473           | 0.322                           | 3659.7                 |
| 636               | TTTTTCTTCGTCGAATGCC   | 780        | 65.26                       | 1.20   | 0.717                | 0.931                          | 0.799           | 0.409                           | 5217.7                 |
| 637               | TTTCTTCGTCGAATGCCA    | 781        | 66.11                       | 1.20   | 0.843                | 0.931                          | 0.877           | 0.569                           | 4659.7                 |
| 638               | TTCTTCGTCGAATGCCAT    | 782        | 65.73                       | 1.00   | 0.787                | 0.757                          | 0.776           | 0.526                           | 4347.7                 |
| 639               | TTCTTCGTCGAATGCCAT    | 783        | 65.73                       | 1.00   | 0.787                | 0.757                          | 0.776           | 0.506                           | 5267.4                 |
| 640               | TTCTTCGTCGAATGCCATG   | 784        | 65.26                       | -0.60  | 0.718                | -0.634                         | 0.204           | 0.246                           | 3922.8                 |
| 641               | CTTCTTCGTCGAATGTT     | 785        | 66.97                       | -1.30  | 0.968                | -1.243                         | 0.128           | 0.246                           | 3608.6                 |
| 642               | TTCTTCGTCGAATGTT      | 786        | 65.36                       | -1.30  | 0.733                | -1.243                         | -0.018          | 0.044                           | 1881.6                 |
| 643               | TTCTTCGTCGAATGTTT     | 787        | 65.36                       | -1.30  | 0.733                | -1.243                         | -0.018          | 0.044                           | 1658.0                 |
| 644               | GTGTCGAATGCCATGTTA    | 788        | 63.32                       | -1.30  | 0.433                | -1.243                         | -0.204          | 0.255                           | 1369.8                 |
| 645               | TTCTTCGAATGCCATGTTTAA | 789        | 59.38                       | -1.30  | -0.144               | -1.243                         | -0.562          | 0.353                           | 605.8                  |
| 646               | GTCAATGCCATGTTTAAAC   | 790        | 59.99                       | -1.30  | -0.055               | -1.243                         | -0.506          | 0.357                           | 933.2                  |
| 647               | TCAATGCCATGTTTAACT    | 791        | 58.93                       | -1.30  | -0.211               | -1.243                         | -0.603          | 0.334                           | 441.8                  |

Table 4

| p5 Probe Position | DNA Probe Sequence  | SEQ ID NO: | RNA/DNA T <sub>m</sub> (°C) | $\Delta G_{\text{fold}}$ (kcal/mole @ 35 °C) | T <sub>m</sub> Score | $\Delta G_{\text{fold}}$ Score | Composite Score | Window-Averaged Composite Score | HIV PRT GeneChip™ Data |
|-------------------|---------------------|------------|-----------------------------|--|----------------------|--------------------------------|-----------------|---------------------------------|------------------------|
| 648               | CAATGGCCATGTTTAACTT | 792        | 57.97                       | -0.90  | -0.352               | -0.895                         | -0.558          | -0.384                          | 545.6                  |
| 649               | AATGGCCATGTTTAACTTT | 793        | 57.07                       | 0.90   | -0.483               | 0.870                          | -0.045          | -0.473                          | 781.4                  |
| 650               | ATGGCCATGTTTAACTTTT | 794        | 59.31                       | 0.90   | -0.156               | 0.870                          | 0.158           | -0.092                          | 1027.3                 |
| 651               | TGGCCATGTTTAACTTTTG | 795        | 59.24                       | 0.90   | -0.165               | 0.870                          | 0.152           | 0.024                           | 1102.5                 |
| 652               | GGCCATGTTTAACTTTTGG | 796        | 61.84                       | 0.30   | 0.216                | 0.149                          | 0.190           | 0.156                           | 935.7                  |
| 653               | CCCATGTTTAACTTTTGGG | 797        | 61.84                       | -0.10  | 0.216                | -0.199                         | 0.058           | 0.218                           | 403.7                  |
| 654               | CAATGTTTAACTTTTGGGC | 798        | 61.84                       | 0.30   | 0.216                | 0.149                          | 0.190           | 0.254                           | 269.3                  |
| 655               | CAATGTTTAACTTTTGGGC | 799        | 61.84                       | 0.30   | 0.216                | 0.149                          | 0.190           | 0.299                           | 296.8                  |
| 656               | ATGTTTAACTTTTGGGCCA | 800        | 61.84                       | 0.90   | 0.216                | 0.870                          | 0.389           | 0.362                           | 449.4                  |
| 657               | TGTTTAACTTTTGGGCCAT | 801        | 61.84                       | 0.90   | 0.216                | 0.870                          | 0.389           | 0.372                           | 448.1                  |
| 658               | TGTTTAACTTTTGGGCATC | 802        | 62.91                       | 0.90   | 0.373                | 0.670                          | 0.486           | 0.340                           | 584.9                  |
| 659               | GTTTAACTTTTGGGCATCC | 803        | 66.73                       | 0.40   | 0.934                | 0.236                          | 0.669           | 0.275                           | 1032.4                 |
| 660               | TTTAACTTTTGGGCATCCA | 804        | 64.79                       | -0.70  | 0.649                | -0.721                         | 0.128           | 0.335                           | 737.8                  |
| 661               | TAACTTTTGGGCATCCAT  | 805        | 64.44                       | -1.20  | 0.598                | -1.156                         | -0.069          | 0.274                           | 950.2                  |
| 662               | TAACTTTTGGGCATCCAT  | 806        | 64.44                       | -1.20  | 0.598                | -1.156                         | -0.069          | 0.340                           | 1308.0                 |
| 663               | AACTTTTGGGCATCCATTC | 807        | 66.42                       | -1.20  | 0.888                | -1.156                         | 0.111           | 0.296                           | 2360.1                 |
| 664               | ACTTTTGGGCATCCATTC  | 808        | 72.21                       | -1.20  | 1.738                | -1.156                         | 0.638           | 0.382                           | 4946.0                 |
| 665               | CTTTTGGGCATCCATTCCT | 809        | 73.53                       | -1.20  | 1.930                | -1.156                         | 0.758           | 0.490                           | 6789.2                 |
| 666               | TTTGGGCATCCATTCCTTG | 810        | 71.49                       | -1.20  | 1.632                | -1.156                         | 0.573           | 0.560                           | 8150.6                 |
| 667               | TTGGGCATCCATTCCTG   | 811        | 73.62                       | -1.20  | 1.945                | -1.156                         | 0.766           | 0.622                           | 7589.0                 |
| 668               | TGGGCATCCATTCCTGGC  | 812        | 77.43                       | -2.80  | 2.504                | -2.547                         | 0.584           | 0.590                           | 13914.0                |
| 669               | TGGGCATCCATTCCTGGCT | 813        | 78.94                       | -3.50  | 2.725                | -3.156                         | 0.490           | 0.500                           | 17513.0                |
| 670               | GGGCATCCATTCCTGGCTT | 814        | 79.51                       | -3.50  | 2.809                | -3.156                         | 0.542           | 0.449                           | 19883.0                |
| 671               | GGCATCCATTCCTGGCTTT | 815        | 77.37                       | -3.50  | 2.494                | -3.156                         | 0.347           | 0.324                           | 20703.0                |
| 672               | GCATCCATTCCTGGCTTTA | 816        | 74.28                       | -3.10  | 2.040                | -2.808                         | 0.198           | 0.214                           | 18622.0                |
| 673               | CATCCATTCCTGGCTTTAA | 817        | 67.92                       | -1.30  | 1.109                | -1.243                         | 0.215           | 0.132                           | 16915.0                |
| 674               | CATCATTCCTGGCTTTAAT | 818        | 64.36                       | -1.30  | 0.585                | -1.243                         | -0.109          | 0.028                           | 13910.0                |

Table 4

| p5 Probe Position | DNA Probe Sequence    | SEQ ID NO: | RNA/DNA T <sub>m</sub> (°C) | $\Delta G_{\text{fold}}$ (kcal/mole @ 35 °C) | T <sub>m</sub> Score | $\Delta G_{\text{fold}}$ Score | Composite Score | Window-Averaged Composite Score | HIV PRT GeneChip™ Data |
|-------------------|-----------------------|------------|-----------------------------|--|----------------------|--------------------------------|-----------------|---------------------------------|------------------------|
| 675               | ATCAATCTCGGCTTAAT     | 819        | 63.53                       | -1.30  | 0.464                | -1.243                         | -0.185          | -0.009                          | 12524.0                |
| 676               | TCATCTCCUGCTTTAATTT   | 820        | 63.88                       | -1.30  | 0.516                | -1.243                         | -0.152          | -0.005                          | 11890.0                |
| 677               | CAATCTCGGCTTTAATTT    | 821        | 62.81                       | -0.90  | 0.359                | -0.895                         | -0.118          | 0.040                           | 12839.0                |
| 678               | CAATCTCGGCTTTAATTTA   | 822        | 58.55                       | 0.90   | -0.266               | 0.670                          | 0.090           | 0.426                           | 9726.8                 |
| 679               | ATTCCTGGCTTTAATTTTAC  | 823        | 57.84                       | 1.50   | -0.371               | 1.192                          | 0.223           | 0.038                           | 8499.7                 |
| 680               | TTCTCGGCTTTAATTTTACT  | 824        | 59.78                       | 1.90   | -0.086               | 1.540                          | 0.532           | 0.336                           | 6800.4                 |
| 681               | TCCTGGCTTTAATTTTACTG  | 825        | 59.37                       | 1.90   | -0.146               | 1.540                          | 0.494           | 0.306                           | 5445.6                 |
| 682               | CTGCGCTTTAATTTTACTGG  | 826        | 60.53                       | 1.90   | 0.024                | 1.540                          | 0.800           | 0.434                           | 2901.6                 |
| 683               | CTGCGCTTTAATTTTACTGGT | 827        | 59.77                       | 1.90   | -0.087               | 1.540                          | 0.531           | 0.434                           | 1174.2                 |
| 684               | TGGCTTTAATTTTACTGGTAC | 828        | 57.25                       | 1.90   | -0.458               | 1.540                          | 0.301           | 0.268                           | 521.3                  |
| 685               | GCTTTAATTTTACTGGTAC   | 829        | 57.86                       | 1.90   | -0.368               | 1.540                          | 0.357           | 0.065                           | 611.1                  |
| 686               | GCTTTAATTTTACTGGTAC   | 830        | 58.55                       | 1.80   | -0.560               | 1.453                          | 0.205           | -0.148                          | 287.6                  |
| 687               | CTTTAATTTTACTGGTACAG  | 831        | 52.66                       | 0.40   | -1.130               | 0.236                          | -0.611          | -0.330                          | 109.5                  |
| 688               | TTAATTTTACTGGTACAGT   | 832        | 53.62                       | -0.80  | -0.989               | -0.808                         | -0.920          | -0.464                          | 59.5                   |
| 689               | TTAATTTTACTGGTACAGTC  | 833        | 54.59                       | -1.00  | -0.599               | -0.982                         | -0.898          | -0.540                          | 62.1                   |
| 690               | TAATTTTACTGGTACAGTCT  | 834        | 56.28                       | -1.00  | -0.599               | -0.982                         | -0.745          | -0.632                          | 59.4                   |
| 691               | TAATTTTACTGGTACAGTC   | 835        | 58.27                       | -1.00  | -0.308               | -0.982                         | -0.564          | -0.613                          | 68.0                   |
| 692               | ATTTTACTGGTACAGTCTCA  | 836        | 61.78                       | -1.00  | 0.207                | -0.982                         | -0.245          | -0.561                          | 72.9                   |
| 693               | TTTACTGGTACAGTCTCAA   | 837        | 59.61                       | -1.00  | -0.111               | -0.982                         | -0.442          | -0.615                          | 62.2                   |
| 694               | TTTACTGGTACAGTCTCAAT  | 838        | 59.25                       | -1.00  | -0.164               | -0.982                         | -0.475          | -0.439                          | 64.5                   |
| 695               | TTTACTGGTACAGTCTCAATA | 839        | 58.30                       | -1.00  | -0.303               | -0.982                         | -0.561          | -0.318                          | 53.5                   |
| 696               | TACTGGTACAGTCTCAATAG  | 840        | 58.15                       | -1.00  | -0.326               | -0.982                         | -0.575          | -0.166                          | 57.8                   |
| 697               | CTGGTACAGTCTCAATAGG   | 841        | 61.44                       | -0.80  | 0.157                | -0.808                         | -0.210          | 0.034                           | 341.0                  |
| 698               | CTGGTACAGTCTCAATAGG   | 842        | 63.55                       | 0.10   | 0.467                | -0.025                         | 0.280           | 0.186                           | 54.8                   |
| 699               | TGGTACAGTCTCAATAGGCG  | 843        | 65.89                       | 1.10   | 0.810                | 0.844                          | 0.823           | 0.279                           | 47.1                   |
| 700               | GGTACAGTCTCAATAGGCT   | 844        | 68.08                       | 0.90   | 1.131                | 0.670                          | 0.956           | 0.383                           | 59.7                   |
| 701               | GTCAGTCTCAATAGGCTA    | 845        | 64.73                       | 0.70   | 0.640                | 0.496                          | 0.586           | 0.425                           | 47.0                   |

Table 4

| p5 Probe Position | DNA Probe Sequence  | SEQ ID NO: | RNA/DNA $T_m$ (°C) | $\Delta G_{\text{fold}}$ (kcal/mole @ 35 °C) | $T_m$ Score | $\Delta G_{\text{fold}}$ Score | Composite Score | Window-Averaged Composite Score | HIV PRT GeneChip™ Data |
|-------------------|---------------------|------------|--------------------|--|-------------|--------------------------------|-----------------|---------------------------------|------------------------|
| 702               | TACAGTCTCAATAGGCTAA | 846        | 59.35              | 0.70   | -0.149      | 0.496                          | 0.096           | 0.425                           | 49.3                   |
| 703               | ACAGTCTCAATAGGCTAA  | 847        | 59.91              | 0.70   | -0.067      | 0.496                          | 0.147           | 0.388                           | 55.0                   |
| 704               | CAGTCTCAATAGGCTAATG | 848        | 59.29              | 0.70   | -0.158      | 0.496                          | 0.091           | 0.225                           | 49.0                   |
| 705               | AGTCTCAATAGGCTAATGG | 849        | 60.62              | 0.90   | 0.037       | 0.670                          | 0.278           | 0.229                           | 45.7                   |
| 706               | GTCTCAATAGGCTAATGG  | 850        | 63.00              | 1.10   | 0.386       | 0.844                          | 0.560           | 0.189                           | 115.6                  |
| 707               | TCTCAATAGGCTAATGGGA | 851        | 61.22              | 0.40   | 0.125       | 0.236                          | 0.167           | 0.133                           | 50.6                   |
| 708               | CTCAATAGGCTAATGGGAA | 852        | 57.97              | 1.40   | -0.352      | 1.105                          | 0.202           | 0.025                           | 48.0                   |
| 709               | TCATAGGCTAATGGGAAA  | 853        | 54.39              | 1.40   | -0.877      | 1.105                          | -0.124          | -0.008                          | 50.5                   |
| 710               | CAATAGGCTAATGGGAAA  | 854        | 51.64              | 1.80   | -1.281      | 1.453                          | -0.242          | -0.191                          | 44.1                   |
| 711               | AATAGGCTAATGGGAAAT  | 855        | 50.45              | 1.90   | -1.454      | 1.540                          | -0.316          | -0.298                          | 43.1                   |
| 712               | ATAGGCTAATGGGAAATTT | 856        | 52.34              | 1.00   | -1.178      | 0.757                          | -0.442          | -0.432                          | 45.2                   |
| 713               | TAGGCTAATGGGAAATTT  | 857        | 52.63              | 0.50   | -1.135      | 0.323                          | -0.581          | -0.560                          | 47.4                   |
| 714               | AGGCTAATGGGAAATTTA  | 858        | 52.63              | 0.50   | -1.135      | 0.323                          | -0.581          | -0.747                          | 50.0                   |
| 715               | GGCTAATGGGAAATTTAA  | 859        | 50.89              | 0.50   | -1.390      | 0.323                          | -0.739          | -0.867                          | 47.8                   |
| 716               | GCCTAATGGGAAATTTAAA | 860        | 47.14              | 0.50   | -1.940      | 0.323                          | -1.080          | -1.022                          | 50.2                   |
| 717               | GCTAATGGGAAATTTAAG  | 861        | 45.00              | 0.50   | -2.254      | 0.323                          | -1.275          | -1.096                          | 43.0                   |
| 718               | CTAATGGGAAATTTAAGT  | 862        | 43.95              | 0.50   | -2.408      | 0.323                          | -1.371          | -1.098                          | 57.0                   |
| 719               | TATGGGAAATTTAAGTG   | 863        | 42.27              | 0.50   | -2.655      | 0.323                          | -1.524          | -1.072                          | 58.7                   |
| 720               | AATGGGAAATTTAAGTGC  | 864        | 46.18              | 0.70   | -2.081      | 0.496                          | -1.102          | -1.011                          | 183.6                  |
| 721               | ATGGGAAATTTAAGTGCA  | 865        | 48.90              | 1.70   | -1.692      | 1.366                          | -0.524          | -0.924                          | 303.4                  |
| 722               | TGGGAAATTTAAGTGCA   | 866        | 47.39              | 1.80   | -1.903      | 1.453                          | -0.628          | -0.837                          | 135.7                  |
| 723               | GGGAAATTTAAGTGCAC   | 867        | 47.84              | 1.60   | -1.838      | 1.279                          | -0.653          | -0.766                          | 241.7                  |
| 724               | GGAATTTAAGTGCAC     | 868        | 49.12              | 1.20   | -1.649      | 0.931                          | -0.669          | -0.737                          | 132.5                  |
| 725               | GAATTTAAGTGCACCA    | 869        | 48.09              | 1.20   | -1.801      | 0.931                          | -0.763          | -0.758                          | 128.8                  |
| 726               | AAATTTAAGTGCACCA    | 870        | 45.57              | 1.10   | -2.171      | 0.844                          | -1.025          | -0.720                          | 141.0                  |
| 727               | AAATTTAAGTGCACCAT   | 871        | 46.97              | 1.10   | -1.965      | 0.844                          | -0.897          | -0.629                          | 282.0                  |
| 728               | AATTTAAGTGCACCAATC  | 872        | 49.46              | 1.10   | -1.599      | 0.844                          | -0.671          | -0.620                          | 948.6                  |

Table 4

| p5 Probe Position | DNA Probe Sequence   | SEQ ID NO: | RNA/DNA T <sub>m</sub> (°C) | $\Delta G_{\text{fold}}$ (kcal/mole @ 35 °C) | T <sub>m</sub> Score | $\Delta G_{\text{fold}}$ Score | Composite Score | Window-Averaged Composite Score | HIV PRT GeneChip™ Data |
|-------------------|----------------------|------------|-----------------------------|--|----------------------|--------------------------------|-----------------|---------------------------------|------------------------|
| 729               | ATTTAAGTGCACCAATCT   | 873        | 52.84                       | 1.10   | -1.104               | 0.844                          | -0.363          | -0.567                          | 1815.1                 |
| 730               | TTTAAAGTGCACCAATCTG  | 874        | 52.81                       | 1.10   | -1.109               | 0.844                          | -0.366          | -0.426                          | 3185.2                 |
| 731               | TTAAAGTGCACCAATCTGA  | 875        | 53.71                       | 1.00   | -0.976               | 0.757                          | -0.317          | -0.263                          | 3566.1                 |
| 732               | TAAAGTGCACCAATCTGAG  | 876        | 53.56                       | 1.00   | -0.999               | 0.757                          | -0.331          | -0.087                          | 2925.1                 |
| 733               | AAAGTGCACCAATCTGAGT  | 877        | 56.81                       | 1.00   | -0.522               | 0.757                          | -0.036          | 0.014                           | 3233.2                 |
| 734               | AAGTGCACCAATCTGAGTC  | 878        | 59.99                       | 1.00   | -0.055               | 0.757                          | 0.254           | 0.085                           | 3615.6                 |
| 735               | AGTGCACCAATCTGAGTCA  | 879        | 63.25                       | 1.00   | 0.422                | 0.757                          | 0.550           | 0.465                           | 3994.8                 |
| 736               | GTGCACCAATCTGAGTCAA  | 880        | 61.00                       | 1.00   | 0.083                | 0.757                          | 0.345           | 0.138                           | 4033.0                 |
| 737               | TGCACCAATCTGAGTCAAC  | 881        | 58.82                       | 1.00   | -0.257               | 0.757                          | 0.128           | 0.008                           | 3380.2                 |
| 738               | GACCAATCTGAGTCAACA   | 882        | 59.87                       | 1.00   | -0.073               | 0.757                          | 0.242           | -0.173                          | 4288.7                 |
| 739               | CAACCAATCTGAGTCAACG  | 883        | 56.22                       | -0.30  | -0.608               | -0.373                         | -0.519          | -0.445                          | 744.1                  |
| 740               | AACCAATCTGAGTCAACGA  | 884        | 56.24                       | -1.60  | -0.605               | -1.504                         | -0.946          | -0.757                          | 392.2                  |
| 741               | ACCAATCTGAGTCAACGAT  | 885        | 58.10                       | -2.30  | -0.332               | -2.112                         | -1.009          | -1.030                          | 158.1                  |
| 742               | CCAATCTGAGTCAACGATT  | 886        | 57.90                       | -3.30  | -0.362               | -2.982                         | -1.357          | -1.279                          | 70.8                   |
| 743               | CAATCTGAGTCAACGATTT  | 887        | 54.41                       | -3.80  | -0.874               | -3.417                         | -1.840          | -1.262                          | 190.0                  |
| 744               | ATCTGAGTCAACGATTTTC  | 888        | 54.37                       | -3.60  | -0.880               | -3.243                         | -1.778          | -1.168                          | 87.7                   |
| 745               | ATCTGAGTCAACGATTTCT  | 889        | 58.37                       | -2.60  | -0.293               | -2.373                         | -1.084          | -1.077                          | 152.7                  |
| 746               | TCTGATCAACGATTTCTT   | 890        | 58.73                       | -1.90  | -0.241               | -1.764                         | -0.820          | -0.797                          | 270.5                  |
| 747               | CTGAGTCAACGATTTCTTC  | 891        | 58.73                       | -0.30  | -0.241               | -0.373                         | -0.291          | -0.553                          | 498.7                  |
| 748               | TGATCAACGATTTCTTCC   | 892        | 60.70                       | 0.20   | 0.049                | 0.062                          | 0.054           | -0.324                          | 891.0                  |
| 749               | GAGTCAACGATTTCTTCCA  | 893        | 62.06                       | 0.20   | 0.248                | 0.062                          | 0.177           | -0.224                          | 1509.8                 |
| 750               | ATCAACGATTTCTTCCAA   | 894        | 58.66                       | 0.20   | -0.250               | 0.062                          | -0.132          | -0.482                          | 1099.3                 |
| 751               | GTCAACGATTTCTTCCAAT  | 895        | 58.47                       | 0.20   | -0.279               | 0.062                          | -0.149          | -0.235                          | 1198.0                 |
| 752               | TCAACGATTTCTTCCAATT  | 896        | 55.86                       | 0.20   | -0.661               | 0.062                          | -0.367          | -0.345                          | 680.5                  |
| 753               | CAACGATTTCTTCCAATTA  | 897        | 54.08                       | 0.20   | -0.922               | 0.062                          | -0.548          | -0.384                          | 762.5                  |
| 754               | ACGAGATTTCTTCCAATTAT | 898        | 52.82                       | 0.20   | -1.107               | 0.062                          | -0.683          | -0.445                          | 689.8                  |
| 755               | ACGATTTCTTCCAATTATG  | 899        | 54.58                       | 0.20   | -0.849               | 0.062                          | -0.503          | -0.445                          | 715.1                  |

Table 4

| p5 Probe Position | DNA Probe Sequence    | SEQ ID NO: | RNA/DNA $T_m$ (°C) | $\Delta G_{fold}$ (kcal/mole @ 35 °C) | $T_m$ Score | $\Delta G_{fold}$ Score | Composite Score | Window-Averaged Composite Score | HIV PRT GeneChip™ Data |
|-------------------|-----------------------|------------|--------------------|---------------------------------------|-------------|-------------------------|-----------------|---------------------------------|------------------------|
| 756               | CAGATTTCTTCCAAATATGT  | 900        | 56.99              | 0.20                                  | -0.498      | 0.062                   | -0.284          | -0.460                          | 833.8                  |
| 757               | AGATTTCTTCCAAATATGT   | 901        | 56.02              | 0.20                                  | -0.638      | 0.062                   | -0.372          | -0.445                          | 1067.7                 |
| 758               | GATTTCTTCCAAATATGTG   | 902        | 55.80              | 0.30                                  | -0.670      | 0.149                   | -0.359          | -0.401                          | 1225.9                 |
| 759               | ATTTCTTCCAAATATGTGA   | 903        | 55.80              | -0.10                                 | -0.670      | -0.199                  | -0.491          | -0.382                          | 1028.7                 |
| 760               | TTTCTTCCAAATATGTGAC   | 904        | 56.34              | -0.10                                 | -0.591      | -0.199                  | -0.442          | -0.328                          | 1419.0                 |
| 761               | TTCTTCCAAATATGTGACA   | 905        | 57.29              | -0.10                                 | -0.452      | -0.199                  | -0.356          | -0.348                          | 1437.4                 |
| 762               | CTCTTCCAAATATGTGACAG  | 906        | 57.14              | -0.10                                 | -0.474      | -0.199                  | -0.369          | -0.325                          | 1518.3                 |
| 763               | CTTCCAAATATGTGACAGG   | 907        | 58.36              | -0.10                                 | -0.295      | -0.199                  | -0.259          | -0.262                          | 1560.3                 |
| 764               | TCCAAATATGTGACAGGT    | 908        | 59.43              | -0.10                                 | -0.138      | -0.199                  | -0.161          | -0.244                          | 1100.0                 |
| 765               | CCAAATATGTGACAGGTG    | 909        | 59.02              | -0.10                                 | -0.198      | -0.199                  | -0.198          | -0.216                          | 1096.4                 |
| 766               | CAATATATGTGACAGGTGT   | 910        | 60.68              | -0.10                                 | 0.046       | -0.199                  | -0.047          | -0.124                          | 1103.4                 |
| 767               | CAATATATGTGACAGGTGTA  | 911        | 56.24              | 0.30                                  | -0.605      | 0.149                   | -0.319          | -0.065                          | 738.1                  |
| 768               | AAATATATGTGACAGGTGTAG | 912        | 55.09              | 1.10                                  | -0.774      | 0.844                   | -0.159          | 0.054                           | 596.7                  |
| 769               | ATTATATGTGACAGGTGTAGG | 913        | 59.83              | 1.10                                  | -0.079      | 0.844                   | 0.272           | 0.161                           | 548.1                  |
| 770               | TTATATGTGACAGGTGTAGGT | 914        | 63.16              | 1.10                                  | 0.409       | 0.844                   | 0.575           | 0.274                           | 701.1                  |
| 771               | TATATGTGACAGGTGTAGGTC | 915        | 64.38              | -0.20                                 | 0.588       | -0.286                  | 0.256           | 0.420                           | 724.7                  |
| 772               | ATGTGACAGGTGTAGGTCC   | 916        | 69.08              | -0.60                                 | 1.278       | -0.634                  | 0.551           | 0.506                           | 1129.8                 |
| 773               | TTGTGACAGGTGTAGGTCTCT | 917        | 71.21              | -0.60                                 | 1.591       | -0.634                  | 0.745           | 0.537                           | 1214.0                 |
| 774               | GTGACAGGTGTAGGTCTCTA  | 918        | 70.75              | -0.60                                 | 1.523       | -0.634                  | 0.703           | 0.520                           | 1425.4                 |
| 775               | TTGACAGGTGTAGGTCTCTAC | 919        | 67.83              | -0.60                                 | 1.095       | -0.634                  | 0.438           | 0.499                           | 838.8                  |
| 776               | GACAGGTGTAGGTCTCTACT  | 920        | 69.52              | -0.90                                 | 1.343       | -0.895                  | 0.493           | 0.427                           | 1173.1                 |
| 777               | GACAGGTGTAGGTCTACTA   | 921        | 69.06              | -0.90                                 | 1.275       | -0.895                  | 0.450           | 0.304                           | 1367.0                 |
| 778               | ACAGGTGTAGGTCTACTTAA  | 922        | 65.30              | -0.90                                 | 0.723       | -0.895                  | 0.108           | 0.192                           | 877.0                  |
| 779               | CAGGTGTAGGTCTACTTAAT  | 923        | 64.69              | -0.90                                 | 0.634       | -0.895                  | 0.053           | 0.100                           | 897.6                  |
| 780               | AGGTGTAGGTCTACTTAATA  | 924        | 62.84              | -0.90                                 | 0.362       | -0.895                  | -0.115          | -0.024                          | 962.2                  |
| 781               | GGTGTAGGTCTACTTAATAC  | 925        | 63.19              | -0.90                                 | 0.414       | -0.895                  | -0.083          | -0.000                          | 1382.6                 |
| 782               | GTGTAGGTCTACTTAATACT  | 926        | 62.53              | -0.90                                 | 0.317       | -0.895                  | -0.143          | -0.000                          | 1132.9                 |

Table 4

| p5 Probe Position | DNA Probe Sequence     | SEQ ID NO: | RNA/DNA T <sub>m</sub> (°C) | $\Delta G_{fold}$ (kcal/mole @ 35 °C) | T <sub>m</sub> Score | $\Delta G_{fold}$ Score | Composite Score | Window-Averaged Composite Score | HIV PRT GeneChip™ Data |
|-------------------|------------------------|------------|-----------------------------|---------------------------------------|----------------------|-------------------------|-----------------|---------------------------------|------------------------|
| 783               | GTGAGTCTCTACTAATCTAG   | 927        | 59.27                       | -0.90                                 | -0.160               | -0.895                  | -0.439          | -0.095                          | 1180.7                 |
| 784               | GTAGTCTCTACTAATCTAGT   | 928        | 62.53                       | -0.50                                 | 0.317                | -0.547                  | -0.011          | -0.020                          | 1932.9                 |
| 785               | TAGTCTCTACTAATCTACTGA  | 929        | 58.77                       | 0.70                                  | -0.234               | 0.496                   | 0.043           | 0.042                           | 1634.4                 |
| 786               | AGTCTCTACTAATCTACTGAC  | 930        | 59.91                       | 0.50                                  | -0.067               | 0.323                   | 0.081           | 0.062                           | 2488.1                 |
| 787               | GGTCTCTACTAATCTACTGACC | 931        | 63.54                       | 0.50                                  | 0.466                | 0.323                   | 0.411           | 0.416                           | 3580.9                 |
| 788               | GTCTCTACTAATCTACTGACT  | 932        | 62.91                       | 0.50                                  | 0.373                | 0.323                   | 0.354           | 0.048                           | 3850.1                 |
| 789               | TCCTCTACTAATCTACTGACTA | 933        | 58.31                       | 0.50                                  | -0.155               | 0.323                   | 0.026           | -0.044                          | 1879.0                 |
| 790               | CTCTACTAATCTACTGACTAT  | 934        | 57.99                       | 0.50                                  | -0.348               | 0.323                   | -0.093          | -0.063                          | 1920.4                 |
| 791               | CTACTAATCTACTGACTATA   | 935        | 53.68                       | 0.50                                  | -0.981               | 0.323                   | -0.486          | -0.094                          | 1131.2                 |
| 792               | TACTAATCTACTGACTATAG   | 936        | 51.92                       | 0.70                                  | -1.240               | 0.496                   | -0.580          | -0.147                          | 786.5                  |
| 793               | ACTAATCTACTGACTATAGC   | 937        | 56.45                       | 1.20                                  | -0.574               | 0.931                   | -0.002          | -0.142                          | 1881.3                 |
| 794               | CTAATCTACTGACTATAGCT   | 938        | 57.85                       | 1.20                                  | -0.369               | 0.931                   | 0.125           | -0.102                          | 2033.6                 |
| 795               | TATCTACTGACTATAGCTT    | 939        | 56.25                       | 1.20                                  | -0.604               | 0.931                   | -0.021          | -0.005                          | 1853.9                 |
| 796               | AATCTACTGACTATAGCTTT   | 940        | 57.14                       | 1.20                                  | -0.473               | 0.931                   | 0.050           | 0.411                           | 2462.6                 |
| 797               | ATCTCTACTATAGCTTTA     | 941        | 58.55                       | 1.20                                  | -0.266               | 0.931                   | 0.189           | 0.183                           | 2436.8                 |
| 798               | TACTCTACTATAGCTTTAT    | 942        | 58.55                       | 1.20                                  | -0.266               | 0.931                   | 0.189           | 0.220                           | 1885.2                 |
| 799               | ACTCTACTATAGCTTTATG    | 943        | 59.06                       | 1.20                                  | -0.192               | 0.931                   | 0.235           | 0.331                           | 1682.1                 |
| 800               | CTGTACTCTAGCTTTATGT    | 944        | 61.64                       | 1.30                                  | 0.187                | 1.018                   | 0.503           | 0.405                           | 1551.3                 |
| 801               | TGTACTCTAGCTTTATGTC    | 945        | 61.08                       | 1.10                                  | 0.105                | 0.844                   | 0.386           | 0.484                           | 1600.1                 |
| 802               | GTACTCTAGCTTTATGTCC    | 946        | 66.16                       | 1.10                                  | 0.703                | 0.844                   | 0.757           | 0.522                           | 4094.6                 |
| 803               | TACTCTAGCTTTATGTCCA    | 947        | 63.16                       | 1.10                                  | 0.409                | 0.844                   | 0.575           | 0.562                           | 2794.2                 |
| 804               | ACCTCTAGCTTTATGTCCAC   | 948        | 64.30                       | 1.30                                  | 0.577                | 1.018                   | 0.745           | 0.675                           | 4754.9                 |
| 805               | CCCTAGCTTTATGTCCACA    | 949        | 64.94                       | 1.30                                  | 0.671                | 1.018                   | 0.803           | 0.564                           | 4185.4                 |
| 806               | CTAAGCTTTATGTCCACAG    | 950        | 61.34                       | 1.10                                  | 0.143                | 0.844                   | 0.409           | 0.484                           | 3284.3                 |
| 807               | TATAGCTTTATGTCCACAGA   | 951        | 60.70                       | 1.10                                  | 0.048                | 0.844                   | 0.351           | 0.453                           | 2819.7                 |
| 808               | ATCTCTAGCTTTATGTCCAGAT | 952        | 61.27                       | 0.60                                  | 0.132                | 0.410                   | 0.238           | 0.414                           | 3545.1                 |
| 809               | TAGCTTTATGTCCACAGATT   | 953        | 61.63                       | 0.60                                  | 0.186                | 0.410                   | 0.271           | 0.337                           | 4232.6                 |

Table 4

| p5 Probe Position | DNA Probe Sequence    | SEQ ID NO: | RNA/DNA $T_m$ (°C) | $\Delta G_{MFO}$ (kcal/mole @ 35 °C) | $T_m$ Score | $\Delta G_{MFO}$ Score | Composite Score | Window-Averaged Composite Score | HIV PRT GeneChip™ Data |
|-------------------|-----------------------|------------|--------------------|--------------------------------------|-------------|------------------------|-----------------|---------------------------------|------------------------|
| 810               | ACCTTATGTCTCCACAGATT  | 954        | 62.57              | 0.60                                 | 0.324       | 0.410                  | 0.356           | 0.283                           | 5252.8                 |
| 811               | GCTTATGTCTCCACAGATT   | 955        | 63.85              | 0.60                                 | 0.511       | 0.410                  | 0.472           | 0.233                           | 6823.9                 |
| 812               | CTTATGTCTCCACAGATTCT  | 956        | 61.56              | 0.60                                 | 0.176       | 0.410                  | 0.265           | 0.193                           | 4829.8                 |
| 813               | TTTATGTCTCCACAGATTCTA | 957        | 58.97              | 0.60                                 | -0.205      | 0.410                  | 0.029           | 0.143                           | 4333.7                 |
| 814               | TATGTCTCCACAGATTCTAT  | 958        | 58.62              | 0.60                                 | -0.257      | 0.410                  | -0.004          | 0.144                           | 3801.0                 |
| 815               | TATGTCTCCACAGATTCTATG | 959        | 58.20              | 0.60                                 | -0.318      | 0.410                  | -0.041          | 0.142                           | 3528.2                 |
| 816               | ATGTCTCCACAGATTCTATGA | 960        | 60.12              | 0.60                                 | -0.036      | 0.410                  | 0.134           | 0.159                           | 2080.0                 |
| 817               | TGTCTCCACAGATTCTATGAG | 961        | 60.34              | 0.60                                 | -0.004      | 0.410                  | 0.153           | 0.145                           | 913.8                  |
| 818               | GTCTCCACAGATTCTATGAGT | 962        | 63.68              | 0.60                                 | 0.486       | 0.410                  | 0.457           | 0.192                           | 1228.3                 |
| 819               | TCTCCACAGATTCTATGAGTA | 963        | 59.83              | 0.80                                 | -0.078      | 0.583                  | 0.173           | 0.062                           | 238.1                  |
| 820               | CCACAGATTCTATGAGTAT   | 964        | 58.43              | 1.10                                 | -0.285      | 0.844                  | 0.144           | -0.028                          | 219.4                  |
| 821               | CACAGATTCTATGAGTATC   | 965        | 55.78              | 0.90                                 | -0.673      | 0.670                  | -0.162          | -0.169                          | 138.6                  |
| 822               | ACAGATTCTATGAGTATCT   | 966        | 56.48              | -0.10                                | -0.571      | -0.199                 | -0.430          | -0.273                          | 112.7                  |
| 823               | ACAGATTCTATGAGTATCTG  | 967        | 55.85              | -1.30                                | -0.663      | -1.243                 | -0.883          | -0.322                          | 133.8                  |
| 824               | AGATTCTATGAGTATCTGA   | 968        | 55.87              | -0.10                                | -0.659      | -0.199                 | -0.485          | -0.392                          | 296.8                  |
| 825               | GATTCTATGAGTATCTGAT   | 969        | 55.69              | 0.60                                 | -0.686      | 0.410                  | -0.270          | -0.442                          | 279.7                  |
| 826               | ATTCTATGAGTATCTGATC   | 970        | 55.67              | 0.80                                 | -0.689      | 0.583                  | -0.206          | -0.498                          | 484.4                  |
| 827               | TTTCTATGAGTATCTGATCA  | 971        | 57.06              | 0.20                                 | -0.485      | 0.082                  | -0.277          | -0.540                          | 502.0                  |
| 828               | TCTATGAGTATCTGATCAT   | 972        | 56.70              | -0.50                                | -0.538      | -0.547                 | -0.541          | -0.569                          | 637.3                  |
| 829               | TCATGAGTATCTGATCATTA  | 973        | 55.75              | -1.10                                | -0.678      | -1.069                 | -0.826          | -0.652                          | 489.0                  |
| 830               | CTATGAGTATCTGATCATAC  | 974        | 54.95              | -1.30                                | -0.794      | -1.243                 | -0.965          | -0.742                          | 808.7                  |
| 831               | TATGAGTATCTGATCATACT  | 975        | 54.95              | -1.10                                | -0.794      | -1.069                 | -0.899          | -0.738                          | 903.2                  |
| 832               | ATGAGTATCTGATCATACTG  | 976        | 55.49              | -1.20                                | -0.715      | -1.156                 | -0.883          | -0.702                          | 1709.3                 |
| 833               | TGAGTATCTGATCATACTGT  | 977        | 58.64              | -1.20                                | -0.254      | -1.156                 | -0.597          | -0.604                          | 2103.9                 |
| 834               | GAGTATCTGATCATACTGTC  | 978        | 60.20              | -1.20                                | -0.025      | -1.156                 | -0.455          | -0.468                          | 3973.4                 |
| 835               | AGTATCTGATCATACTGCT   | 979        | 60.88              | -1.00                                | 0.076       | -0.982                 | -0.326          | -0.330                          | 6462.3                 |
| 836               | GATCTGATCATACTGCTTT   | 980        | 61.03              | -0.30                                | 0.097       | -0.373                 | -0.081          | -0.462                          | 9749.0                 |

Table 4

| p5 Probe Position | DNA Probe Sequence   | SEQ ID NO: | RNA/DNA T <sub>m</sub> (°C) | $\Delta G_{\text{fold}}$ (kcal/mole @ 35 °C) | T <sub>m</sub> Score | $\Delta G_{\text{fold}}$ Score | Composite Score | Window-Averaged Composite Score | HIV PRT GeneChip™ Data |
|-------------------|----------------------|------------|-----------------------------|--|----------------------|--------------------------------|-----------------|---------------------------------|------------------------|
| 837               | TATCTGATCATGCTGCTTGA | 981        | 57.16                       | 0.90   | -0.470               | 0.670                          | -0.037          | -0.059                          | 7817.2                 |
| 838               | ATCTGATCATGCTGCTTAC  | 982        | 58.34                       | 0.90   | -0.298               | 0.670                          | 0.070           | 0.007                           | 9683.1                 |
| 839               | TCTGATCATGCTGCTTACT  | 983        | 60.42                       | 0.90   | 0.008                | 0.670                          | 0.259           | 0.055                           | 8089.0                 |
| 840               | CTGATCATGCTGCTTACTT  | 984        | 59.32                       | 0.90   | -0.164               | 0.670                          | 0.159           | 0.067                           | 8696.8                 |
| 841               | TGATCATGCTGCTTACTTTG | 985        | 57.63                       | 0.90   | -0.401               | 0.670                          | 0.006           | 0.064                           | 8680.5                 |
| 842               | GATCATGCTGCTTACTTTG  | 986        | 57.63                       | 0.90   | -0.401               | 0.670                          | 0.006           | 0.020                           | 7033.7                 |
| 843               | ATCATGCTGCTTACTTTGA  | 987        | 57.63                       | 0.90   | -0.401               | 0.670                          | 0.008           | -0.003                          | 5406.5                 |
| 844               | TCTGCTGCTTACTTTGAT   | 988        | 57.63                       | 0.70   | -0.401               | 0.496                          | -0.060          | -0.215                          | 4239.4                 |
| 845               | CATGCTGCTTACTTTGATA  | 989        | 55.68                       | 0.70   | -0.688               | 0.496                          | -0.238          | -0.328                          | 3727.4                 |
| 846               | ATGCTGCTTACTTTGATGA  | 990        | 52.44                       | 0.70   | -1.163               | 0.496                          | -0.533          | -0.660                          | 2665.5                 |
| 847               | TACTGCTTACTTTGATAAA  | 991        | 50.65                       | 0.70   | -1.426               | 0.496                          | -0.696          | -0.696                          | 1817.8                 |
| 848               | ACTGCTTACTTTGATAAA   | 992        | 49.49                       | -0.30  | -1.595               | -0.373                         | -1.131          | -0.809                          | 1335.9                 |
| 849               | CTGCTTACTTTGATAAAC   | 993        | 49.49                       | -0.50  | -1.595               | -0.547                         | -1.197          | -0.916                          | 1526.2                 |
| 850               | TGCTTACTTTGATAAACC   | 994        | 51.45                       | -0.50  | -1.309               | -0.547                         | -1.019          | -0.949                          | 822.7                  |
| 851               | GTCTTACTTTGATAAAGT   | 995        | 53.32                       | -0.50  | -1.034               | -0.547                         | -0.849          | -0.966                          | 1227.4                 |
| 852               | TCTTACTTTGATAAAGCTC  | 996        | 51.75                       | -0.50  | -1.264               | -0.547                         | -0.991          | -0.946                          | 503.0                  |
| 853               | CTTACTTTGATAAAGCTCC  | 997        | 54.28                       | -0.50  | -0.894               | -0.547                         | -0.762          | -0.910                          | 1174.3                 |
| 854               | TTACTTTGATAAAGCTCCA  | 998        | 53.70                       | -0.50  | -0.978               | -0.547                         | -0.814          | -0.901                          | 885.5                  |
| 855               | TACTTTGATAAAGCTCGA   | 999        | 51.79                       | -0.50  | -1.259               | -0.547                         | -0.988          | -0.916                          | 660.6                  |
| 856               | ACTTTGATAAAGCTCCGAT  | 1000       | 52.29                       | -0.50  | -1.185               | -0.547                         | -0.943          | -0.826                          | 615.4                  |
| 857               | CTTTGATAAAGCTCGAAT   | 1001       | 52.11                       | -0.50  | -1.212               | -0.547                         | -0.959          | -0.728                          | 563.4                  |
| 858               | TGTGATAAAGCTCGAATTC  | 1002       | 51.46                       | -0.30  | -1.307               | -0.373                         | -0.952          | -0.664                          | 420.9                  |
| 859               | TTGATAAAGCTCGAATTC   | 1003       | 54.68                       | 0.60   | -0.834               | 0.410                          | -0.362          | -0.398                          | 536.6                  |
| 860               | TGATAAAGCTCGAATTC    | 1004       | 57.79                       | 0.60   | -0.378               | 0.410                          | -0.079          | -0.022                          | 1417.8                 |
| 861               | GATAAAGCTCGAATTC     | 1005       | 61.15                       | 1.00   | 0.114                | 0.757                          | 0.359           | 0.258                           | 4351.2                 |
| 862               | ATAAAGCTCGAATTC      | 1006       | 63.24                       | 1.90   | 0.421                | 1.540                          | 0.846           | 0.560                           | 7738.7                 |
| 863               | TAAAGCTCGAATTC       | 1007       | 64.88                       | 1.90   | 0.663                | 1.540                          | 0.996           | 0.847                           | 11136.0                |

Table 4

| p5 Probe Position | DNA Probe Sequence     | SEQ ID NO: | RNA/DNA $T_m$ (°C) | $\Delta G_{\text{Mfold}}$ (kcal/mole @ 35 °C) | $T_m$ Score | $\Delta G_{\text{Mfold}}$ Score | Composite Score | Window-Averaged Composite Score | HIV PRT GeneChip™ Data |
|-------------------|------------------------|------------|--------------------|---|-------------|---------------------------------|-----------------|---------------------------------|------------------------|
| 864               | AAACCTCGAATTCGCCCTA    | 1008       | 64.88              | 1.90  | 0.863       | 1.540                           | 0.996           | 1.074                           | 14811.0                |
| 865               | AAACCTCGAATTCGCCCTAT   | 1009       | 66.73              | 1.90  | 0.933       | 1.540                           | 1.164           | 1.261                           | 15751.0                |
| 866               | AACCTCGAATTCGCCCTATC   | 1010       | 70.07              | 1.80  | 1.424       | 1.453                           | 1.435           | 1.330                           | 19861.0                |
| 867               | ACCTCGAATTCGCCCTATCA   | 1011       | 73.21              | 1.80  | 1.883       | 1.453                           | 1.720           | 1.335                           | 20370.0                |
| 868               | CCCTCGAATTCGCCCTATCAT  | 1012       | 72.84              | 1.80  | 1.801       | 1.453                           | 1.669           | 1.327                           | 19376.0                |
| 869               | CTCGAATTCGCCCTATCATTT  | 1013       | 69.66              | 1.60  | 1.364       | 1.279                           | 1.332           | 1.254                           | 17642.0                |
| 870               | TCCGAATTCGCCCTATCATTTT | 1014       | 68.21              | 1.10  | 1.150       | 0.844                           | 1.034           | 1.093                           | 13751.0                |
| 871               | CGAATTCGCCCTATCATTTT   | 1015       | 67.12              | 1.10  | 0.991       | 0.844                           | 0.935           | 0.931                           | 12669.0                |
| 872               | CAATTCGCCCTATCATTTT    | 1016       | 64.02              | 1.10  | 0.536       | 0.844                           | 0.653           | 0.848                           | 9255.9                 |
| 873               | AATTCGCCCTATCATTTTGG   | 1017       | 62.80              | 0.40  | 0.357       | 0.236                           | 0.311           | 0.753                           | 8929.1                 |
| 874               | ATTCGCCCTATCATTTTGG    | 1018       | 67.28              | 0.00  | 1.014       | -0.112                          | 0.586           | 0.745                           | 6148.2                 |
| 875               | TTCCGCCCTATCATTTTGGT   | 1019       | 70.46              | 0.00  | 1.480       | -0.112                          | 0.875           | 0.664                           | 5468.0                 |
| 876               | TCCGCCCTATCATTTTGGTT   | 1020       | 70.46              | 0.00  | 1.480       | -0.112                          | 0.875           | 0.653                           | 5803.7                 |
| 877               | CCCCCTATCATTTTGGTTT    | 1021       | 69.27              | 0.00  | 1.307       | -0.112                          | 0.768           | 0.658                           | 5192.0                 |
| 878               | CCCTATCATTTTGGTTTTC    | 1022       | 67.18              | 0.00  | 1.000       | -0.112                          | 0.577           | 0.549                           | 3557.4                 |
| 879               | CCCTATCATTTTGGTTTCC    | 1023       | 67.18              | 0.00  | 1.000       | -0.112                          | 0.577           | 0.392                           | 5274.3                 |
| 880               | CCATCATTTTGGTTTCCA     | 1024       | 64.63              | 0.00  | 0.625       | -0.112                          | 0.345           | 0.270                           | 3787.9                 |
| 881               | CTATCATTTTGGTTTCCAT    | 1025       | 60.77              | -0.50   | 0.059       | -0.547                          | -0.171          | 0.162                           | 2726.8                 |
| 882               | TATCATTTTGGTTTCCATC    | 1026       | 60.20              | -0.50   | -0.025      | -0.547                          | -0.223          | 0.092                           | 3249.9                 |
| 883               | ATCATTTTGGTTTCCATCT    | 1027       | 62.83              | -0.50   | 0.361       | -0.547                          | 0.016           | 0.061                           | 5548.9                 |
| 884               | CAATTTTGGTTTCCATCTT    | 1028       | 63.21              | -0.50   | 0.416       | -0.547                          | 0.050           | 0.024                           | 5290.0                 |
| 885               | CAATTTTGGTTTCCATCTTC   | 1029       | 63.21              | -0.50   | 0.416       | -0.547                          | 0.050           | 0.152                           | 7451.0                 |
| 886               | ATTTTGGTTTCCATCTTCC    | 1030       | 65.88              | -0.50   | 0.809       | -0.547                          | 0.293           | 0.262                           | 11578.0                |
| 887               | TTTTGGTTTCCATCTTCTT    | 1031       | 67.93              | -0.50   | 1.109       | -0.547                          | 0.480           | 0.366                           | 13722.0                |
| 888               | TTTTGGTTTCCATCTCTCG    | 1032       | 67.42              | -0.50   | 1.035       | -0.547                          | 0.434           | 0.425                           | 15064.0                |
| 889               | TTTGGTTTCCATCTTCTCG    | 1033       | 69.71              | -0.90   | 1.370       | -0.895                          | 0.508           | 0.554                           | 10869.0                |
| 890               | TTGGTTTCCATCTTCTGCG    | 1034       | 73.74              | -1.30   | 1.962       | -1.243                          | 0.744           | 0.535                           | 16035.0                |

Table 4

| p5 Probe Position | DNA Probe Sequence   | SEQ ID NO: | RNA/DNA T <sub>m</sub> (°C) | $\Delta G_{\text{fold}}$ (kcal/mole @ 35 °C) | T <sub>m</sub> Score | $\Delta G_{\text{fold}}$ Score | Composite Score | Window-Averaged Composite Score | HIV PRT GeneChip™ Data |
|-------------------|----------------------|------------|-----------------------------|--|----------------------|--------------------------------|-----------------|---------------------------------|------------------------|
| 891               | TGCTTCCATCTCTCTGCA   | 1035       | 74.48                       | -1.30  | 2.071                | -1.243                         | 0.812           | 0.452                           | 16304.0                |
| 892               | GGTTTCATCTCTCTGGCA   | 1036       | 72.21                       | -1.30  | 1.737                | -1.243                         | 0.605           | 0.406                           | 14885.0                |
| 893               | GGTTTCATCTCTCTGGCAA  | 1037       | 67.37                       | -1.30  | 1.027                | -1.243                         | 0.165           | 0.358                           | 11910.0                |
| 894               | TTCATCTCTCTCTGGCAAC  | 1038       | 64.82                       | -1.30  | 0.853                | -1.243                         | -0.087          | 0.300                           | 11929.0                |
| 895               | TTCCATCTCTCTGGCAACT  | 1039       | 66.34                       | -1.30  | 0.877                | -1.243                         | 0.071           | 0.252                           | 11517.0                |
| 896               | TCATCTCTCTGGCAACTC   | 1040       | 67.47                       | -1.30  | 1.042                | -1.243                         | 0.174           | 0.232                           | 11822.0                |
| 897               | CATCTCTCTGGCAACTCA   | 1041       | 67.12                       | -0.90  | 0.991                | -0.895                         | 0.274           | 0.285                           | 11710.0                |
| 898               | CATCTCTCTGGCAACTCAT  | 1042       | 63.55                       | 0.90   | 0.466                | 0.670                          | 0.544           | 0.352                           | 7635.3                 |
| 899               | ATCTCTCTGGCAACTCATT  | 1043       | 62.71                       | 1.00   | 0.343                | 0.757                          | 0.501           | 0.406                           | 8378.2                 |
| 900               | TCTCTCTGGCAACTCATTT  | 1044       | 63.06                       | 0.90   | 0.395                | 0.670                          | 0.500           | 0.446                           | 6321.4                 |
| 901               | CTCTCTGGCAACTCATTTTC | 1045       | 63.06                       | 0.70   | 0.395                | 0.496                          | 0.434           | 0.468                           | 7659.0                 |
| 902               | TCTCTGGCAACTCATTTCT  | 1046       | 63.06                       | 0.70   | 0.395                | 0.496                          | 0.434           | 0.436                           | 11621.0                |
| 903               | TCTCTGGCAACTCATTTCTT | 1047       | 63.06                       | 0.70   | 0.395                | 0.496                          | 0.434           | 0.363                           | 3389.0                 |
| 904               | CTGGCAACTCATTTCTTC   | 1048       | 63.06                       | 0.70   | 0.395                | 0.496                          | 0.434           | 0.273                           | 3870.6                 |
| 905               | CTGGCAACTCATTTCTTCT  | 1049       | 61.24                       | 0.70   | 0.127                | 0.496                          | 0.288           | 0.160                           | 1992.7                 |
| 906               | TGGCAACTCATTTCTCTTA  | 1050       | 58.74                       | 0.70   | -0.239               | 0.496                          | 0.040           | -0.046                          | 698.3                  |
| 907               | GGCAACTCATTTCTCTTAA  | 1051       | 56.86                       | 0.70   | -0.514               | 0.496                          | -0.130          | -0.204                          | 718.3                  |
| 908               | GCAACTCATTTCTCTTAAT  | 1052       | 54.36                       | 0.70   | -0.882               | 0.496                          | -0.368          | -0.336                          | 372.3                  |
| 909               | CAACTCATTTCTCTTAATA  | 1053       | 49.93                       | 0.60   | -1.530               | 0.410                          | -0.793          | -0.430                          | 180.6                  |
| 910               | AACTCATTTCTCTTAATAC  | 1054       | 49.11                       | 0.80   | -1.651               | 0.410                          | -0.868          | -0.456                          | 430.0                  |
| 911               | ACTCATTTCTCTTAATACT  | 1055       | 52.79                       | 0.60   | -1.111               | 0.410                          | -0.533          | -0.484                          | 904.3                  |
| 912               | ACTCATTTCTCTTAATAGT  | 1056       | 54.63                       | 0.60   | -0.842               | 0.410                          | -0.366          | -0.540                          | 1653.5                 |
| 913               | CTCATTTCTCTTAATAGT   | 1057       | 57.14                       | 0.80   | -0.474               | 0.410                          | -0.138          | -0.459                          | 2694.2                 |
| 914               | CTATTTCTCTTAATAGTGA  | 1058       | 54.51                       | 0.60   | -0.859               | 0.410                          | -0.377          | -0.364                          | 3222.9                 |
| 915               | CATTTCTCTTAATAGTAT   | 1059       | 53.21                       | 0.60   | -1.049               | 0.410                          | -0.495          | -0.340                          | 3142.8                 |
| 916               | ATTCTCTCTTAATAGTATC  | 1060       | 53.13                       | 0.80   | -1.081               | 0.583                          | -0.436          | -0.270                          | 5867.0                 |
| 917               | TTTCTCTCTTAATAGTATCA | 1061       | 54.51                       | 1.20   | -0.859               | 0.931                          | -0.179          | -0.263                          | 6641.4                 |

Table 4

| p5 Probe Position | DNA Probe Sequence    | SEQ ID NO: | RNA/DNA $T_m$ (°C) | $\Delta G_{\text{fold}}$ (kcal/mole @ 35 °C) | $T_m$ Score | $\Delta G_{\text{fold}}$ Score | Composite Score | Window-Averaged Composite Score | HIV PRT GeneChip™ Data |
|-------------------|-----------------------|------------|--------------------|--|-------------|--------------------------------|-----------------|---------------------------------|------------------------|
| 918               | TCTCTCTAATACATGATCAT  | 1062       | 54.17              | 1.30   | -0.908      | 1.018                          | -0.176          | -0.229                          | 7151.9                 |
| 919               | TCTCTAATACATGATCATC   | 1063       | 55.17              | 1.30   | -0.762      | 1.018                          | -0.086          | -0.439                          | 8134.9                 |
| 920               | CTTCTAATACATGATCATCT  | 1064       | 55.86              | 1.30   | -0.661      | 1.018                          | -0.023          | -0.448                          | 8551.4                 |
| 921               | TCTTAATACATGATCATG    | 1065       | 53.80              | 1.30   | -0.964      | 1.018                          | -0.211          | -0.003                          | 5741.7                 |
| 922               | TCTTAATACATGATCATCTGC | 1066       | 57.65              | 1.30   | -0.398      | 1.018                          | 0.140           | 0.404                           | 8575.9                 |
| 923               | CTAATACATGATCATCTGCT  | 1067       | 58.28              | 1.30   | -0.307      | 1.018                          | 0.197           | 0.248                           | 8980.3                 |
| 924               | TAAATACATGATCATCTGCTC | 1068       | 57.85              | 1.30   | -0.398      | 1.018                          | 0.140           | 0.394                           | 10762.0                |
| 925               | AATACATGATCATCTGCTCC  | 1069       | 62.19              | 1.30   | 0.268       | 1.018                          | 0.553           | 0.566                           | 17037.0                |
| 926               | ATACTGATCATCTGCTCCT   | 1070       | 66.43              | 1.30   | 0.889       | 1.018                          | 0.938           | 0.682                           | 20970.0                |
| 927               | TACTGATCATCTGCTCCG    | 1071       | 66.32              | 1.30   | 0.874       | 1.018                          | 0.929           | 0.763                           | 23084.0                |
| 928               | ACTGATCATCTGCTCCTGT   | 1072       | 70.36              | 0.60   | 1.466       | 0.410                          | 1.065           | 0.875                           | 24474.0                |
| 929               | CTGTATCATCTGCTCCTGTA  | 1073       | 69.13              | 0.60   | 1.286       | 0.410                          | 0.953           | 0.910                           | 22217.0                |
| 930               | TGTATCATCTGCTCCTGTAT  | 1074       | 67.04              | 0.60   | 0.979       | 0.410                          | 0.763           | 0.890                           | 19829.0                |
| 931               | GTATCATCTGCTCCTGTATC  | 1075       | 68.85              | 0.60   | 1.244       | 0.410                          | 0.927           | 0.842                           | 23548.0                |
| 932               | TATCATCTGCTCCTGTATCT  | 1076       | 67.44              | 0.60   | 1.037       | 0.410                          | 0.799           | 0.723                           | 21759.0                |
| 933               | ATCATCTGCTCCTGTATCTA  | 1077       | 67.44              | 0.60   | 1.037       | 0.410                          | 0.799           | 0.725                           | 22711.0                |
| 934               | TATCTGCTCCTGTATCTTAA  | 1078       | 65.13              | 0.60   | 0.699       | 0.410                          | 0.589           | 0.706                           | 18134.0                |
| 935               | CATCTGCTCCTGTATCTAAT  | 1079       | 63.60              | 1.00   | 0.475       | 0.757                          | 0.582           | 0.644                           | 17772.0                |
| 936               | ATCTGCTCCTGTATCTAATA  | 1080       | 61.77              | 1.60   | 0.207       | 1.279                          | 0.614           | 0.502                           | 17134.0                |
| 937               | TCTGCTCCTGTATCTAATAG  | 1081       | 62.01              | 1.60   | 0.241       | 1.279                          | 0.635           | 0.389                           | 10969.0                |
| 938               | CTGCTCCTGTATCTAATAGA  | 1082       | 61.90              | 0.50   | 0.225       | 0.323                          | 0.262           | 0.336                           | 9556.3                 |
| 939               | TGCTCCTGTATCTAATAGAG  | 1083       | 60.12              | 0.30   | -0.036      | 0.149                          | 0.034           | 0.284                           | 3739.9                 |
| 940               | GCTCCTGTATCTAATAGAGC  | 1084       | 64.50              | -1.00  | 0.607       | -0.982                         | 0.003           | 0.187                           | 4088.3                 |
| 941               | CTCCTGTATCTAATAGAGCT  | 1085       | 62.21              | 0.30   | 0.271       | 0.149                          | 0.224           | 0.406                           | 2263.0                 |
| 942               | TCTGTATCTAATAGAGCTT   | 1086       | 60.56              | 0.30   | 0.028       | 0.149                          | 0.074           | 0.080                           | 1018.0                 |
| 943               | CTGTATCTAATAGAGCTTC   | 1087       | 60.56              | 0.30   | 0.028       | 0.149                          | 0.074           | 0.064                           | 1319.1                 |
| 944               | CTGTATCTAATAGAGCTTCC  | 1088       | 60.56              | 0.30   | 0.028       | 0.149                          | 0.074           | 0.070                           | 2347.8                 |

Table 4

| p5 Probe Position | DNA Probe Sequence    | SEQ ID NO: | RNA/DNA $T_m$ (°C) | $\Delta G_{MFOLD}$ (kcal/mole @ 35 °C) | $T_m$ Score | $\Delta G_{MFOLD}$ Score | Composite Score | Window-Averaged Composite Score | HIV PRT GeneChip™ Data |
|-------------------|-----------------------|------------|--------------------|--|-------------|--------------------------|-----------------|---------------------------------|------------------------|
| 945               | TGTACTATATAGAGCTTCCT  | 1089       | 60.55              | 0.30                                   | 0.028       | 0.149                    | 0.074           | 0.048                           | 1871.6                 |
| 946               | GTAATCTATAGAGCTTCCT   | 1090       | 61.00              | 0.30                                   | 0.092       | 0.149                    | 0.114           | -0.040                          | 3469.1                 |
| 947               | TATCTATATAGAGCTTCCT   | 1091       | 58.20              | 0.30                                   | -0.318      | 0.149                    | -0.141          | -0.030                          | 1114.6                 |
| 948               | ATCTATATAGAGCTTCCT    | 1092       | 58.20              | 0.30                                   | -0.318      | 0.149                    | -0.141          | -0.052                          | 1358.4                 |
| 949               | CTATATAGAGCTTCCTTTAG  | 1093       | 58.39              | 0.30                                   | -0.289      | 0.149                    | -0.123          | -0.028                          | 665.4                  |
| 950               | CTAATAGAGCTTCCTTTAGT  | 1094       | 60.12              | 0.00                                   | -0.036      | -0.112                   | -0.065          | -0.049                          | 807.4                  |
| 951               | TATATAGAGCTTCCTTTAGTT | 1095       | 58.46              | 0.30                                   | -0.280      | 0.149                    | -0.117          | -0.138                          | 608.7                  |
| 952               | AATAGAGCTTCCTTTAGTTG  | 1096       | 58.97              | 0.30                                   | -0.205      | 0.149                    | -0.070          | 0.332                           | 623.8                  |
| 953               | ATAGAGCTTCCTTTAGTTGC  | 1097       | 65.53              | 0.30                                   | 0.758       | 0.149                    | 0.526           | 0.526                           | 874.5                  |
| 954               | TAGAGCTTCCTTTAGTTGCC  | 1098       | 69.50              | 0.30                                   | 1.340       | 0.149                    | 0.887           | 0.841                           | 814.3                  |
| 955               | GAGCTTCCTTTAGTTGCC    | 1099       | 73.89              | 0.30                                   | 1.983       | 0.149                    | 1.286           | 1.157                           | 1183.8                 |
| 956               | GAGCTTCCTTTAGTTGCC    | 1100       | 77.20              | 0.30                                   | 2.470       | 0.149                    | 1.588           | 1.454                           | 2219.4                 |
| 957               | AGCTTCCTTTAGTTGCC     | 1101       | 79.38              | 0.30                                   | 2.789       | 0.149                    | 1.785           | 1.650                           | 4642.2                 |
| 958               | GCTTCCTTTAGTTGCC      | 1102       | 82.41              | 0.40                                   | 3.234       | 0.236                    | 2.095           | 1.765                           | 8804.8                 |
| 959               | CTTCCTTTAGTTGCC       | 1103       | 80.06              | 0.80                                   | 2.889       | 0.583                    | 2.013           | 1.823                           | 11331.0                |
| 960               | TTCTTCCTTTAGTTGCC     | 1104       | 77.67              | 1.10                                   | 2.539       | 0.844                    | 1.895           | 1.818                           | 12976.0                |
| 961               | TCTTCCTTTAGTTGCC      | 1105       | 77.27              | 0.80                                   | 2.480       | 0.410                    | 1.693           | 1.765                           | 12369.0                |
| 962               | CTTTCCTTTAGTTGCC      | 1106       | 77.27              | 0.80                                   | 2.480       | 0.410                    | 1.693           | 1.669                           | 15090.0                |
| 963               | CTTTTCCTTTAGTTGCC     | 1107       | 75.74              | 0.80                                   | 2.255       | 0.410                    | 1.554           | 1.581                           | 16130.0                |
| 964               | TTTTCCTTTAGTTGCC      | 1108       | 74.23              | 0.80                                   | 2.033       | 0.410                    | 1.416           | 1.545                           | 15304.0                |
| 965               | TTCCTTTAGTTGCC        | 1109       | 74.23              | 0.60                                   | 2.033       | 0.410                    | 1.416           | 1.539                           | 14829.0                |
| 966               | TTCCTTTAGTTGCC        | 1110       | 73.31              | 0.80                                   | 1.899       | 0.583                    | 1.399           | 1.490                           | 15309.0                |
| 967               | TTTCCTTTAGTTGCC       | 1111       | 73.83              | 1.40                                   | 1.976       | 1.105                    | 1.645           | 1.498                           | 15205.0                |
| 968               | TTTCCTTTAGTTGCC       | 1112       | 73.91              | 1.40                                   | 1.986       | 1.105                    | 1.652           | 1.524                           | 14192.0                |
| 969               | TTTCCTTTAGTTGCC       | 1113       | 70.59              | 1.40                                   | 1.500       | 1.105                    | 1.350           | 1.515                           | 8699.5                 |
| 970               | TTTCCTTTAGTTGCC       | 1114       | 73.39              | 1.40                                   | 1.911       | 1.105                    | 1.605           | 1.461                           | 7786.6                 |
| 971               | TTTCCTTTAGTTGCC       | 1115       | 73.39              | 1.40                                   | 1.911       | 1.105                    | 1.605           | 1.328                           | 6709.1                 |

Table 4

| p5 Probe Position | DNA Probe Sequence     | SEQ ID NO: | RNA/DNA T <sub>m</sub> (°C) | $\Delta G_{fold}$ (kcal/mole @ 35 °C) | T <sub>m</sub> Score | $\Delta G_{fold}$ Score | Composite Score | Window-Averaged Composite Score | HIV PRT GeneChip™ Data |
|-------------------|------------------------|------------|-----------------------------|---------------------------------------|----------------------|-------------------------|-----------------|---------------------------------|------------------------|
| 972               | CCCCCTATCTTTATTGTGA    | 1116       | 70.61                       | 1.40                                  | 1.502                | 1.105                   | 1.351           | 1.165                           | 6198.4                 |
| 973               | CCCCCTATCTTTATTGTGAC   | 1117       | 67.66                       | 1.20                                  | 1.070                | 0.931                   | 1.017           | 0.999                           | 4910.2                 |
| 974               | CCCCCTATCTTTATTGTGAGC  | 1118       | 64.37                       | 1.20                                  | 0.587                | 0.931                   | 0.718           | 0.780                           | 850.0                  |
| 975               | CCCCCTATCTTTATTGTGACGA | 1119       | 62.05                       | 1.20                                  | 0.248                | 0.931                   | 0.507           | 0.670                           | 404.9                  |
| 976               | CCATCTCTTTATTGTGACGAG  | 1120       | 58.56                       | 1.20                                  | -0.265               | 0.931                   | 0.190           | 0.436                           | 166.6                  |
| 977               | CTATCTTTATTGTGACGAGG   | 1121       | 57.28                       | 1.20                                  | -0.452               | 0.931                   | 0.073           | 0.378                           | 126.9                  |
| 978               | TATCTTTATTGTGACGAGGG   | 1122       | 57.91                       | 1.20                                  | -0.361               | 0.931                   | 0.130           | 0.279                           | 92.6                   |
| 979               | ATCTTTATTGTGACGAGGGG   | 1123       | 61.03                       | 1.20                                  | 0.097                | 0.931                   | 0.414           | 0.423                           | 97.9                   |
| 980               | TCTTTATTGTGACGAGGGGT   | 1124       | 64.18                       | 0.90                                  | 0.559                | 0.670                   | 0.601           | 0.602                           | 122.3                  |
| 981               | CTTTATTGTGACGAGGGGTC   | 1125       | 64.18                       | -0.80                                 | 0.559                | -0.908                  | 0.039           | 0.043                           | 267.0                  |
| 982               | TTTATTGTGACGAGGGGTCT   | 1126       | 62.63                       | -1.20                                 | 0.332                | -1.156                  | -0.233          | -0.073                          | 396.0                  |
| 983               | TATTTGTGACGAGGGGTCTT   | 1127       | 65.37                       | -2.30                                 | 0.734                | -2.112                  | -0.348          | -0.146                          | 446.0                  |
| 984               | TATTTGTGACGAGGGGTCTT   | 1128       | 65.37                       | -2.80                                 | 0.734                | -2.547                  | -0.513          | -0.202                          | 661.9                  |
| 985               | ATTGTGACGAGGGGTCTTTG   | 1129       | 65.82                       | -2.80                                 | 0.800                | -2.547                  | -0.472          | -0.163                          | 864.5                  |
| 986               | TTGTGACGAGGGGTCTTTGC   | 1130       | 70.01                       | -2.80                                 | 1.414                | -2.547                  | -0.091          | -0.156                          | 1465.7                 |
| 987               | TGTGACGAGGGGTCTTTGCC   | 1131       | 73.21                       | -2.80                                 | 1.884                | -2.547                  | 0.200           | -0.152                          | 2836.9                 |
| 988               | GTGACGAGGGGTCTTTGCCA   | 1132       | 74.44                       | -2.80                                 | 2.065                | -2.547                  | 0.312           | -0.132                          | 3589.7                 |
| 989               | TGACGAGGGGTCTTTGCCAA   | 1133       | 69.05                       | -2.80                                 | 1.274                | -2.547                  | -0.178          | -0.058                          | 2100.4                 |
| 990               | GACGAGGGGTCTTTGCCAAA   | 1134       | 67.10                       | -2.80                                 | 0.988                | -2.547                  | -0.355          | 0.042                           | 1948.7                 |
| 991               | ACGAGGGGTCTTTGCCAAG    | 1135       | 66.13                       | -2.80                                 | 0.845                | -2.373                  | -0.378          | 0.435                           | 1384.3                 |
| 992               | CGAGGGGTCTTTGCCAAAAG   | 1136       | 66.81                       | -1.40                                 | 0.945                | -1.330                  | 0.081           | 0.482                           | 1192.0                 |
| 993               | GAGGGGTCTTTGCCAAAAGAG  | 1137       | 66.84                       | 0.20                                  | 0.950                | 0.062                   | 0.612           | 0.304                           | 1221.0                 |
| 994               | AGGGGTCTTTGCCAAAAGGT   | 1138       | 68.70                       | 0.20                                  | 1.223                | 0.062                   | 0.782           | 0.437                           | 953.2                  |
| 995               | GGGGGTCTTTGCCAAAAGTGS  | 1139       | 68.32                       | 0.20                                  | 1.167                | 0.062                   | 0.747           | 0.546                           | 988.6                  |
| 996               | GGGGGTCTTTGCCAAAAGTGA  | 1140       | 67.11                       | 0.20                                  | 0.989                | 0.062                   | 0.636           | 0.426                           | 937.8                  |
| 997               | GGGTCTTTGCCAAAAGTGTAT  | 1141       | 64.59                       | 0.50                                  | 0.620                | 0.323                   | 0.507           | 0.333                           | 852.1                  |
| 998               | GTCGTTGCCAAAAGTGTATC   | 1142       | 63.51                       | 0.00                                  | 0.461                | -0.112                  | 0.243           | 0.176                           | 1189.4                 |

Table 4

| p5 Probe Position | DNA Probe Sequence   | SEQ ID NO: | RNA/DNA T <sub>m</sub> (°C) | $\Delta G_{\text{mfold}}$ (kcal/mole @ 35 °C) | T <sub>m</sub> Score | $\Delta G_{\text{mfold}}$ Score | Composite Score | Window-Averaged Composite Score | HIV PRT GeneChip™ Data |
|-------------------|----------------------|------------|-----------------------------|---|----------------------|---------------------------------|-----------------|---------------------------------|------------------------|
| 999               | TCGTTCCAAAGAGTGATCT  | 1143       | 62.35                       | -1.00   | 0.291                | -0.982                          | -0.192          | -0.042                          | 1501.7                 |
| 1000              | CGTTGCCAAAGAGTGATCTG | 1144       | 60.92                       | -1.20   | 0.081                | -1.156                          | -0.389          | -0.156                          | 1360.9                 |
| 1001              | GTTCGCAAGAGTGATCTGA  | 1145       | 61.71                       | -1.20   | 0.198                | -1.156                          | -0.317          | -0.263                          | 1112.9                 |
| 1002              | TTCGCAAGAGTGATCTGAG  | 1146       | 58.90                       | -1.20   | -0.215               | -1.156                          | -0.572          | -0.353                          | 488.3                  |
| 1003              | TCCCAAGAGTGATCTGAGG  | 1147       | 61.08                       | -1.20   | 0.104                | -1.156                          | -0.375          | -0.454                          | 400.1                  |
| 1004              | GCCAAAGAGTGATCTGAGG  | 1148       | 63.68                       | -1.50   | 0.485                | -1.417                          | -0.237          | -0.541                          | 401.6                  |
| 1005              | CCAAAGAGTGATCTGAGGA  | 1149       | 60.94                       | -1.20   | 0.084                | -1.156                          | -0.387          | -0.574                          | 199.9                  |
| 1006              | CAAGAGTGATCTGAGGGAA  | 1150       | 55.32                       | -1.20   | -0.741               | -1.156                          | -0.899          | -0.590                          | 202.1                  |
| 1007              | AAAGAGTGATCTGAGGAG   | 1151       | 54.21                       | -1.20   | -0.903               | -1.156                          | -0.999          | -0.491                          | 258.7                  |
| 1008              | AAGAGTGATCTGAGGAGT   | 1152       | 59.12                       | -1.20   | -0.183               | -1.156                          | -0.552          | -0.475                          | 274.7                  |
| 1009              | AGAGTGATCTGAGGAGATT  | 1153       | 61.60                       | -1.00   | 0.181                | -0.982                          | -0.281          | -0.483                          | 297.2                  |
| 1010              | GAGTGATCTGAGGAGATT   | 1154       | 60.78                       | -0.30   | 0.061                | -0.373                          | -0.104          | -0.414                          | 250.6                  |
| 1011              | AGTGATCTGAGGAGTTAA   | 1155       | 57.35                       | 0.60  | -0.443               | 0.410                           | -0.119          | -0.318                          | 231.3                  |
| 1012              | GTGATCTGAGGAGTTAAA   | 1156       | 55.25                       | 0.60  | -0.751               | 0.410                           | -0.310          | -0.286                          | 214.5                  |
| 1013              | TGATCTGAGGAGTTAAAG   | 1157       | 52.55                       | 0.60  | -1.147               | 0.410                           | -0.556          | -0.295                          | 102.3                  |
| 1014              | GAATCTGAGGAGTTAAAGG  | 1158       | 55.09                       | 0.60  | -0.774               | 0.410                           | -0.324          | -0.330                          | 102.3                  |
| 1015              | ATCTGAGGAGTTAAAGGA   | 1159       | 55.09                       | 0.60  | -0.774               | 0.410                           | -0.324          | -0.374                          | 49.4                   |
| 1016              | TCTGAGGAGTTAAAGGAT   | 1160       | 55.09                       | 0.60  | -0.774               | 0.410                           | -0.324          | -0.374                          | 104.3                  |
| 1017              | CTGAGGAGTTAAAGGATA   | 1161       | 53.32                       | 1.00  | -1.034               | 0.757                           | -0.353          | -0.370                          | 46.3                   |
| 1018              | TGAGGAGTTAAAGGATAC   | 1162       | 51.95                       | 1.30  | -1.235               | 1.018                           | -0.378          | -0.360                          | 50.9                   |
| 1019              | GAGGAGTTAAAGGATACA   | 1163       | 53.26                       | 0.90  | -1.043               | 0.670                           | -0.392          |                                 | 58.2                   |
| 1020              | AGGAGTTAAAGGATACAG   | 1164       | 52.14                       | 0.90  | -1.207               | 0.670                           | -0.494          |                                 | 50.5                   |
| 1021              | GGAGTTAAAGGATACAGT   | 1165       | 54.81                       | 0.90  | -0.815               | 0.670                           | -0.251          |                                 | 53.1                   |

Example 3

Synopsis: The method of the present invention is particularly useful as a guide to the iterative refinement of probes. One of the specific predictions made for rabbit  $\beta$ -globin in Example 1 is used to provide an example of such a refinement.

Materials and Methods: The contig spanning positions 5-11 of a portion of the rabbit  $\beta$ -globin gene (Example 1, Table 3) was analyzed, using the experimentally measured data to simulate the results of successive experimental measurements.

The iterative refinement was performed using a rule-based algorithm, outlined below. This algorithm is used by way of example only; other algorithms for efficiently finding local maxima are well known to the art and could be employed to perform this task.

Given experimental data for probes from the 1<sup>st</sup> quartile, median and 3<sup>rd</sup> quartile of a contig, as well as a user-set signal threshold for further consideration of a probe,

- 1) If all 3 measurements are below the user-specified signal threshold, discard the prediction.
- 2) If at least one of the measurements is above the user-specified threshold, determine which point yields the maximum signal.
  - a) If the maximum point is the 1<sup>st</sup> quartile probe, then make three new measurements for probes with the same spacing as that used in the preceding iteration, but displaced so that the third probe is identical to the original 1<sup>st</sup> quartile probe. In other words, repeat the search with the same pattern and spacing, but displace the pattern in the direction of increasing signal found in the first experiment.
  - b) If the maximum point is the 3<sup>rd</sup> quartile probe, then make three new measurements for probes with the same spacing as that used in the preceding iteration, but displaced so that the first probe is identical to the original 3<sup>rd</sup> quartile probe. In other words, repeat the search with the same

pattern and spacing, but displace the pattern in the direction of increasing signal found in the first experiment.

- c) If the maximum point is the median probe, then repeat the experiment, keeping the median point the same, but shrinking the spacing between probes by a factor of 2.

- 3) Continue iteration until a maximum is found, or the user judges the signal level observed to be acceptable. Use the experimental value measured for the probe duplicated in successive iterations to tie together the successive data sets, via a simple normalization procedure, described below. Where appropriate, consider all of the data (i.e. all of the iterations) when deciding how to proceed, or whether the peak hybridization intensity has been found.

Results: Iterative refinement of the contig spanning positions 5-11 in Table 3 proceeds as follows:

*Iteration 1:* Probes are synthesized at positions 6, 8 and 10, yielding the experimental hybridization intensities 180, 220 and 310, respectively.

*Iteration 2:* Following rule 2b), probes are synthesized at positions 10, 12 and 14.

Note that the redundant measurement at position 10 serves as a bridge between experiments, and allows comparison of the two sets by normalizing the intensities by multiplying the second iteration measurements by the ratio of the intensity observed for the probe at position 10 in the first iteration to the value observed in the second iteration. In the simplest case, the ratio is 1; in any case, the second iteration yields the normalized values 310, 390, 240 for probe positions 10, 12 and 14, respectively.

*Iteration 3:* By rule 2c), measurements are performed for probes at positions 11, 12 and 13; after normalization, these yield the normalized hybridization intensities 320, 390 and 410, respectively. Combination of these results with the results from iteration 2, probe position 14, yields the conclusion that the best probe for this intensity peak is the probe that starts at sequence position 13.

The overall result is that iterative improvement converges in three iterations, and requires the synthesis of seven test probes, one of which is the local optimal probe. In addition, the first and second iterations yield probes that exhibit 75% and 95% of the local maximum hybridization intensities, respectively. In many applications, either of these probes would be considered acceptable.

The above examples 1 and 2 demonstrate that two different implementations of the method of the present invention are capable of efficiently predicting regions of high hybridization efficiency in a variety of polynucleotide targets. Many of the predictions yield acceptable probe sequences on the first design iteration, and all would yield optimized probe sets after 2-4 rounds of iterative refinement, as demonstrated in Example 3. The performance demonstrated in these examples greatly exceeds the performance of current methods. Finally, the examples demonstrate that the predictions can be performed by a software application that has been implemented and installed on a Pentium®-based computer workstation.

All publications and patent applications cited in this specification are herein incorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference.

Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, it will be readily apparent to those of ordinary skill in the art in light of the teachings of this invention that certain changes and modifications may be made thereto without departing from the spirit or scope of the appended claims.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Shannon, Karen W.  
Wolber, Paul K.  
Delenstarr, Glenda C.  
Webb, Peter G.  
Kincaid, Robert H.
- (ii) TITLE OF INVENTION: Methods for evaluating oligonucleotide probe sequences
- (iii) NUMBER OF SEQUENCES: 1165
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Records Manager, Legal Department,  
Hewlett-Packard Company M/S 20B0
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  - (C) CITY: Palo Alto
  - (D) STATE: CA
  - (E) COUNTRY: USA
  - (F) ZIP: 94304
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: Not available
  - (B) FILING DATE: 10-FEB-1998
  - (C) CLASSIFICATION: Not available
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Choi, Wendy A.
  - (B) REGISTRATION NUMBER: 36,697
  - (C) REFERENCE/DOCKET NUMBER: 10971464-1
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 650-236-2386
  - (B) TELEFAX: 650-852-8063

(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO

05784674-021501

(ix) FEATURE:  
    (A) NAME/KEY: stem\_loop  
    (B) LOCATION: 2..21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ACTGGCAATC ACAATTGCCA GTAA

24

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 75 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: tRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
    (A) ORGANISM: *Saccharomyces cerevisiae*

(ix) FEATURE:  
    (A) NAME/KEY: tRNA  
    (B) LOCATION: 1..75  
    (C) IDENTIFICATION METHOD: experimental  
    (D) OTHER INFORMATION: /function= "transfer RNA"  
/product= "tRNA-Ala"  
/evidence= EXPERIMENTAL  
/anticodon= (pos: 34 .. 36, aa: Ala)  
/citation= ([1][2])

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    (C) IDENTIFICATION METHOD: experimental  
    (D) OTHER INFORMATION: /evidence= EXPERIMENTAL  
/frequency= 0.9999  
/mod\_base= mlg  
/citation= ([1][2])

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    (A) NAME/KEY: modified\_base  
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    (C) IDENTIFICATION METHOD: experimental  
    (D) OTHER INFORMATION: /evidence= EXPERIMENTAL  
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/mod\_base= d  
/citation= ([1][2])

(ix) FEATURE:  
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    (B) LOCATION: 20  
    (C) IDENTIFICATION METHOD: experimental  
    (D) OTHER INFORMATION: /evidence= EXPERIMENTAL

09704674-001501

/frequency= 0.9999  
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/citation= ([1][2])

(ix) FEATURE:

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- (C) IDENTIFICATION METHOD: experimental
- (D) OTHER INFORMATION: /evidence= EXPERIMENTAL

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/citation= ([1][2])

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- (C) IDENTIFICATION METHOD: experimental
- (D) OTHER INFORMATION: /evidence= EXPERIMENTAL

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/citation= ([1][2])

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- (A) NAME/KEY: modified\_base
- (B) LOCATION: 37
- (C) IDENTIFICATION METHOD: experimental
- (D) OTHER INFORMATION: /evidence= EXPERIMENTAL

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/citation= ([1][2])

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- (A) NAME/KEY: modified\_base
- (B) LOCATION: 38
- (C) IDENTIFICATION METHOD: experimental
- (D) OTHER INFORMATION: /evidence= EXPERIMENTAL

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/mod\_base= p  
/citation= ([1][2])

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- (A) NAME/KEY: modified\_base
- (B) LOCATION: 46
- (C) IDENTIFICATION METHOD: experimental
- (D) OTHER INFORMATION: /evidence= EXPERIMENTAL

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/mod\_base= d  
/citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: modified\_base
- (B) LOCATION: 53
- (C) IDENTIFICATION METHOD: experimental
- (D) OTHER INFORMATION: /evidence= EXPERIMENTAL

/frequency= 0.9999  
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/citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: modified\_base

09784674-021501

(B) LOCATION: 54  
(C) IDENTIFICATION METHOD: experimental  
(D) OTHER INFORMATION: /evidence= EXPERIMENTAL  
/frequency= 0.9999  
/mod\_base= p  
/citation= ([1][2])

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Holley, R. W.  
Apgar, J.  
Everett, G. A.  
Madison, J. T.  
Marquisee, M.  
Merrill, S. H.  
Penswick, J. R.  
Zamir, A.  
(B) TITLE: Structure of a ribonucleic acid  
(C) JOURNAL: Science  
(D) VOLUME: 147  
(F) PAGES: 1462-1465  
(G) DATE: 1965  
(K) RELEVANT RESIDUES IN SEQ ID NO:2: FROM 1 TO 75

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Penswick, J. R.  
Martin, R.  
Dirheimer, G.  
(B) TITLE: Evidence supporting a revised sequence for  
yeast alanine tRNA  
(C) JOURNAL: FEBS Lett.  
(D) VOLUME: 50  
(F) PAGES: 28-31  
(G) DATE: 1975  
(K) RELEVANT RESIDUES IN SEQ ID NO:2: FROM 1 TO 75

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GGGCGUGUGG CGUAGUCGGU AGCGCGCUCC CUUGGCGUGG GAGAGUCUCC GGUUCGAUUC 60  
CGGACUCGUC CACCA 75

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGGACTTAG CATTCG

16

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 12 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

ATGGACTTAG CA

12

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 12 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

TGGACTTAGC AT

12

(2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 12 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

GGACTTAGCA TT

12

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GACTTAGCAT TC

12

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

ACTTAGCATT CG

12

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

00784574-021501

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

GTCCAAAAAG GGTCACTCTA CCTCCGCCA TAAAAAATC ATGTTCAAGA 50

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

GTCCAAAAAG GGTCACTCTA CCTCC 25

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

TCCAAAAAGG GTCAGTCTAC CTCCC 25

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

CCAAAAAGGG TCACTCTACC TCCCG

25

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

CAAAAAGGGT CAGTCTACCT CCCGC

25

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

AAAAAGGGTC AGTCTACCTC CCGCC

25

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

AAAAGGGTCA GTCTACCTCC CGCCA

25

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

AAAGGGTCAG TCTACCTCCC GCCAT

25

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

AAGGGTCAGT CTACCTCCCG CCATA

25

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

03784674-001501

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

AGGGTCAGTC TACCTCCCGC CATAA

25

- (2) INFORMATION FOR SEQ ID NO: 19:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

GGGTCAGTCT ACCTCCCGCC ATAAA

25

- (2) INFORMATION FOR SEQ ID NO: 20:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

GGTCAGTCTA CCTCCCGCCA TAAAA

25

(2) INFORMATION FOR SEQ ID NO: 21:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

GTCAGTCTAC CTCGCGCCAT AAAAA

25

(2) INFORMATION FOR SEQ ID NO: 22:

- (i) SEQUENCE CHARACTERISTICS:
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  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

TCAGTCTACC TCCGCGCCATA AAAAA

25

(2) INFORMATION FOR SEQ ID NO: 23:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

CAGTCTACCT CCGCCATAA AAAAC

25

(2) INFORMATION FOR SEQ ID NO: 24:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

AGTCTACCTC CCGCCATAAA AAAC

25

(2) INFORMATION FOR SEQ ID NO: 25:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

GTCTACCTCC CGCCATAAAA AACTC

25

(2) INFORMATION FOR SEQ ID NO: 26:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

09784674-021504

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

TCTACCTCCC GCCATAAAA ACTCA

25

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 25 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

CTACCTCCCG CCATAAAAA CTCAT

25

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 25 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

TACCTCCCGC CATAAAAAAC TCATG

25

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 25 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

0971464-1 021501

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

ACCTCCCGCC ATAAAAAAT CATGT

25

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

CCTCCCGCCA TAAAAAACTC ATGTT

25

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

CTCCCGCCAT AAAAAACTCA TGTTC

25

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

TCCCGCCATA AAAAATCAT GTTCA

25

(2) INFORMATION FOR SEQ ID NO: 33:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

CCCGCCATAA AAAATCATG TTCAA

25

(2) INFORMATION FOR SEQ ID NO: 34:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

CCGCCATAAA AAATCATGT TCAAG

25

(2) INFORMATION FOR SEQ ID NO: 35:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

CGCCATAAAA AACTCATGTT CAAGA

25

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 122 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Oryctolagus cuniculus*

(ix) FEATURE:

(A) NAME/KEY: 5'UTR

(B) LOCATION: 1..53

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 54..122

(D) OTHER INFORMATION: /codon\_start= 54

/product= "rabbit betal globin, N-terminus"

/citation= ([1])

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Rohrbach, M. L.  
III Johnson, J. E.  
James, M. D.  
Hardison, R. C.

(B) TITLE: Transcriptional unit of the rabbit betal  
globin gene

(C) JOURNAL: Mol. Cell. Biol.

(D) VOLUME: 5

(F) PAGES: 147-160

(G) DATE: 1985

(K) RELEVANT RESIDUES IN SEQ ID NO: 36: FROM 1 TO 122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

ACACTTGCTT TTGACACAAC TGTGTTTACT TGCAATCCCC CAAACAGAC AGA ATG

56

|   |         |     |
|---|---------|-----|
| GTG CAT CTG TCC AGT GAG GAG AAG TCT GCG GTC ACT GCC CTG TGG GGC | Met     |     |
| Val His Leu Ser Ser Glu Glu Lys Ser Ala Val Thr Ala Leu Trp Gly | 1       | 104 |
|   | 5 10 15 |     |
| AAG GTG AAT GTG GAA GAA   |         | 122 |
| Lys Val Asn Val Glu Glu   |         |     |
|   | 20      |     |

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1040 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Human immunodeficiency virus
- (B) STRAIN: type I
- (C) INDIVIDUAL ISOLATE: BH10

(ix) FEATURE:

- (A) NAME/KEY: misc\_RNA
- (B) LOCATION: 1..1040
- (C) IDENTIFICATION METHOD: experimental
- (D) OTHER INFORMATION: /partial

/function= "protease & reverse transcriptase regions"  
/product= "pol polyprotein (partial)"  
/evidence= EXPERIMENTAL  
/citation= ([1])

(x) PUBLICATION INFORMATION:

- (A) AUTHORS: Wong-Stahl, F.  
Gallo, R. C.  
Chang, N. T.  
Ghrayeb, J.  
Papas, T. S.  
Lautenberger, J. A.  
Pearson, M. L.  
Jr. Petteway, S. R.  
Ivanoff, L.  
Baumeister, K.
- (B) TITLE: Complete nucleotide sequence of the AIDS virus, HTLV-III
- (C) JOURNAL: Nature
- (D) VOLUME: 313
- (F) PAGES: 277-284
- (G) DATE: 1985
- (K) RELEVANT RESIDUES IN SEQ ID NO: 37: FROM 1 TO 1040

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

|  |      |
|--|------|
| TGTACTGTCC ATTTATCAGG ATGGAGTTCA TAACCCATCC AAAGGAATGG AGGTTCTTTC  | 60   |
| TGATGTTTTT TGTCTGGTGT GGTAAGTCCC CACCTCAACA GATGTTGTCT CAGCTCCTCT  | 120  |
| ATTTTGTTC TATGCTGCC TATTTCTAAG TCAGATCCTA CATACAAATC ATCCATGTAT    | 180  |
| TGATAGATAA CTATGTCTGG ATTTGTTTT TTAAGAGGCT CTAAGATTTT TGTCATGCTA   | 240  |
| CTTTGGAATA TTGCTGGTGA TCCTTTCCAT CCCTGTGGAA GCACATTGTA CTGATATCTA  | 300  |
| ATCCCTGGTG TCTCATTGTT TATACTAGGT ATGGTAAATG CAGTATACTT CCTGAAGTCT  | 360  |
| TCATCTAAGG GAACTGAAAA ATATGCATCA CCCACATCCA GTACTGTTAC TGATTTTTTC  | 420  |
| TTTTTTAACC CTGCGGGATG TGGTATTCCT AATTGAACTT CCCAGAAGTC TTGAGTTCTC  | 480  |
| TTATTAAGTT CTCTGAAATC TACTAATTTT CTCATTAG TACTGTCTTT TTTCTTTATG    | 540  |
| GCAAACTAGT GAGTATTGTA TGGATTCTCA GGCCCAATTT TTGAAATTTT CCCTTCCTTT  | 600  |
| TCCATTTCTG TACAAATTC TACTAATGCT TTTATTTTTT CTTCGTGCAA TGGCCATTGT   | 660  |
| TTAACTTTTG GGCCATCCAT TCCTGGCTTT AATTTTACTG GTACAGTCTC AATAGGGGCTA | 720  |
| ATGGGAAAAT TTAAGTGCA ACCAATCTGA GTCAACAGAT TTCTTCCAAT TATGTTGACA   | 780  |
| GGTGTAGTGC CTAATAATC TGTACCTATA GCTTTATGTC CACAGATTTT TATGAGTATC   | 840  |
| TGATCATACT GTCTTACTTT GATAAACCT CCAATTCCCC CTATCATTTT TGGTTTCCAT   | 900  |
| CTTCCTGGCA AACTCATTTT TTCTAATACT GTATCATCTG CTCCTGTATC TAATAGAGCT  | 960  |
| TCCTTTAGTT GCCCCCCCTAT CTTTATTGTG ACGAGGGGTC GTTGCCAAAG AGTGATCTGA | 1020 |
| GGGAAGTTAA AGGATACAGT  | 1040 |

(2) INFORMATION FOR SEQ ID NO: 38:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 999 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 1..982
  - (C) IDENTIFICATION METHOD: experimental

(D) OTHER INFORMATION: /partial  
 /codon\_start= 2  
 /function= "glycolysis"  
 /product= "Glyceraldehydephosphate Dehydrogenase"  
 /evidence= EXPERIMENTAL  
 /standard\_name= "G3PDH"  
 /citation= ([1])

(ix) FEATURE:

(A) NAME/KEY: promoter  
 (B) LOCATION: 983..999  
 (D) OTHER INFORMATION: /function= "promoter for T7 RNA polymerase"

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Arcari, P.  
 Martinelli, R.  
 Salvatore, F.  
 (B) TITLE: The complete sequence of a full length cDNA  
 for human liver glyceraldehyde-3-phosphate  
 dehydrogenase: evidence for multiple mRNA species  
 (C) JOURNAL: Nucleic Acids Res.  
 (D) VOLUME: 12  
 (E) ISSUE: 23  
 (F) PAGES: 9179-9189  
 (G) DATE: 1984  
 (K) RELEVANT RESIDUES IN SEQ ID NO: 38: FROM 1 TO 999

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

|   |     |
|---|-----|
| G AAG GTC GGA GTC AAC GGA TTT GGT CGT ATT GGG CGC CTG GTC ACC   | 46  |
| Lys Val Gly Val Asn Gly Phe Gly Arg Ile Gly Arg Leu Val Thr     |     |
| 1 5 10 15   |     |
| AGG GCT GCT TTT AAC TCT GGT AAA GTG GAT ATT GTT GCC ATC AAT GAC | 94  |
| Arg Ala Ala Phe Asn Ser Gly Lys Val Asp Ile Val Ala Ile Asn Asp |     |
| 20 25 30  |     |
| CCC TTC ATT GAC CTC AAC TAC ATG GTT TAC ATG TTC CAA TAT GAT TCC | 142 |
| Pro Phe Ile Asp Leu Asn Tyr Met Val Tyr Met Phe Gln Tyr Asp Ser |     |
| 35 40 45  |     |
| ACC CAT GGC AAA TTC CAT GGC ACC GTC AAG GCT GAG AAC GGG AAG CTT | 190 |
| Thr His Gly Lys Phe His Gly Thr Val Lys Ala Glu Asn Gly Lys Leu |     |
| 50 55 60  |     |
| GTC ATC AAT GGA AAT CCC ATC ACC ATC TTC CAG GAG CGA GAT CCC TCC | 238 |
| Val Ile Asn Gly Asn Pro Ile Thr Ile Phe Gln Glu Arg Asp Pro Ser |     |
| 65 70 75  |     |
| AAA ATC AAG TGG GGC GAT GCT GGC GCT GAG TAC GTC GTG GAG TCC ACT | 286 |
| Lys Ile Lys Trp Gly Asp Ala Gly Ala Glu Tyr Val Val Glu Ser Thr |     |
| 80 85 90 95   |     |
| GGC GTC TTC ACC ACC ATG GAG AAG GCT GGG GCT CAT TTG CAG GGG GGA | 334 |
| Gly Val Phe Thr Thr Met Glu Lys Ala Gly Ala His Leu Gln Gly Gly |     |
| 100 105 110   |     |
| GCC AAA AGG GTC ATC ATC TCT GCC CCC TCT GCT GAT GCC CCC ATG TTC | 382 |

|   |     |
|---|-----|
| Ala Lys Arg Val Ile Ile Ser Ala Pro Ser Ala Asp Ala Pro Met Phe |     |
| 115 120 125   |     |
| GTC ATG GGT GTG AAC CAT GAG AAG TAT GAC AAC AGC CTC AAG ATC ATC | 430 |
| Val Met Gly Val Asn His Glu Lys Tyr Asp Asn Ser Leu Lys Ile Ile |     |
| 130 135 140   |     |
| AGC AAT GCC TCC TGC ACC ACC AAC TGC TTA GCA CCC CTG GCC AAG GTC | 478 |
| Ser Asn Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Leu Ala Lys Val |     |
| 145 150 155   |     |
| ATC CAT GAC AAC TTT GGT ATC GTG GAA GGA CTC ATG ACC ACA GTC CAT | 526 |
| Ile His Asp Asn Phe Gly Ile Val Glu Gly Leu Met Thr Thr Val His |     |
| 160 165 170 175   |     |
| GCC ATC ACT GCC ACC CAG AAG ACT GTG GAT GGC CCC TCC GGG AAA CTG | 574 |
| Ala Ile Thr Ala Thr Gln Lys Thr Val Asp Gly Pro Ser Gly Lys Leu |     |
| 180 185 190   |     |
| TGG CGT GAT GGC CGC GGG GCT CTC CAG AAC ATC ATC CCT GCC TCT ACT | 622 |
| Trp Arg Asp Gly Arg Gly Ala Leu Gln Asn Ile Ile Pro Ala Ser Thr |     |
| 195 200 205   |     |
| GGC GCT GCC AAG GCT GTG GGC AAG GTC ATC CCT GAG CTA GAC GGG AAG | 670 |
| Gly Ala Ala Lys Ala Val Gly Lys Val Ile Pro Glu Leu Asp Gly Lys |     |
| 210 215 220   |     |
| CTC ACT GGC ATG GCC TTC CGT GTC CCC ACT GCC AAC GTG TCA GTG GTG | 718 |
| Leu Thr Gly Met Ala Phe Arg Val Pro Thr Ala Asn Val Ser Val Val |     |
| 225 230 235   |     |
| GAC CTG ACC TGC CGT CTA GAA AAA CCT GCC AAA TAT GAT GAC ATC AAG | 766 |
| Asp Leu Thr Cys Arg Leu Glu Lys Pro Ala Lys Tyr Asp Asp Ile Lys |     |
| 240 245 250 255   |     |
| AAG GTG GTG AAG CAG GCG TCG GAG GGC CCC CTC AAA GGC ATC CTG GGC | 814 |
| Lys Val Val Lys Gln Ala Ser Glu Gly Pro Leu Lys Gly Ile Leu Gly |     |
| 260 265 270   |     |
| TAC ACT GAG CAC CAG GTG GTC TCC TCT GAC TTC AAC AGC GAC ACC CAC | 862 |
| Tyr Thr Glu His Gln Val Val Ser Ser Asp Phe Asn Ser Asp Thr His |     |
| 275 280 285   |     |
| TCC TCC ACC TTT GAC GCT GGG GCT GGC ATT GCC CTC AAC GAC CAC TTT | 910 |
| Ser Ser Thr Phe Asp Ala Gly Ala Gly Ile Ala Leu Asn Asp His Phe |     |
| 290 295 300   |     |
| GTC AAG CTC ATT TCC TGG TAT GAC AAC GAA TTT GGC TAC AGC AAC AGG | 958 |
| Val Lys Leu Ile Ser Trp Tyr Asp Asn Glu Phe Gly Tyr Ser Asn Arg |     |
| 305 310 315   |     |
| GTG GTG GAC CTC ATG GCC CAC ATG CTATAGTGAG TCGTATT              | 999 |
| Val Val Asp Leu Met Ala His Met                                 |     |
| 320 325   |     |

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1049 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(ix) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION: 1..372  
(C) IDENTIFICATION METHOD: experimental  
(D) OTHER INFORMATION: /partial

/codon\_start= 1  
/function= "tumor suppressor"  
/product= "p53 (C-terminal portion)"  
/evidence= EXPERIMENTAL  
/gene= "HSP53G"  
/standard\_name= "p53"

(ix) FEATURE:  
(A) NAME/KEY: 3'UTR  
(B) LOCATION: 373..1049  
(D) OTHER INFORMATION: /citation= ([1])

(x) PUBLICATION INFORMATION:  
(A) AUTHORS: Futreal, P. A.  
Barrett, J. C.  
Wiseman, R. W.  
(B) TITLE: An Alu polymorphism intragenic to the TP53  
gene  
(C) JOURNAL: Nucleic Acids Res.  
(D) VOLUME: 19  
(E) ISSUE: 24  
(F) PAGES: 6977-  
(G) DATE: 1991  
(K) RELEVANT RESIDUES IN SEQ ID NO: 39: FROM 1 TO 1049

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

|   |     |
|---|-----|
| GAG GTG CGT GTT TGT GCC TGT CCT GGG AGA GAC CGG CGC ACA GAG GAA | 48  |
| Glu Val Arg Val Cys Ala Cys Pro Gly Arg Asp Arg Arg Thr Glu Glu |     |
| 1 5 10 15   |     |
| GAG AAT CTC CGC AAG AAA GGG GAG CCT CAC CAC GAG CTG CCC CCA GGG | 96  |
| Glu Asn Leu Arg Lys Lys Gly Glu Pro His His Glu Leu Pro Pro Gly |     |
| 20 25 30  |     |
| AGC ACT AAG CGA GCA CTG CCC AAC AAC ACC AGC TCC TCT CCC CAG CCA | 144 |
| Ser Thr Lys Arg Ala Leu Pro Asn Asn Thr Ser Ser Ser Pro Gln Pro |     |
| 35 40 45  |     |
| AAG AAG AAA CCA CTG GAT GGA GAA TAT TTC ACC CTT CAG ATC CGT GGG | 192 |
| Lys Lys Lys Pro Leu Asp Gly Glu Tyr Phe Thr Leu Gln Ile Arg Gly |     |
| 50 55 60  |     |

|  |      |
|--|------|
| CGT GAG CGC TTC GAG ATG TTC CGA GAG CTG AAT GAG GCC TTG GAA CTC    | 240  |
| Arg Glu Arg Phe Glu Met Phe Arg Glu Leu Asn Glu Ala Leu Glu Leu    |      |
| 65 70 75 80  |      |
| AAG GAT GCC CAG GCT GGG AAG GAG CCA GGG GGG AGC AGG GCT CAC TCC    | 288  |
| Lys Asp Ala Gln Ala Gly Lys Glu Pro Gly Gly Ser Arg Ala His Ser    |      |
| 85 90 95   |      |
| AGC CAC CTG AAG TCC AAA AAG GGT CAG TCT ACC TCC CGC CAT AAA AAA    | 336  |
| Ser His Leu Lys Ser Lys Lys Gly Gln Ser Thr Ser Arg His Lys Lys    |      |
| 100 105 110  |      |
| CTC ATG TTC AAG ACA GAA GGG CCT GAC TCA GAC TGA CATTCTCCAC         | 382  |
| Leu Met Phe Lys Thr Glu Gly Pro Asp Ser Asp *                      |      |
| 115 120  |      |
| TTCTTGTTC CCACGTGACAG CCTCCCTCCC CCATCTCTCC CTCCCCTGCC ATTTTGGGTT  | 442  |
| TTGGGTCTTT GAACCCCTGC TTGCAATAGG TGTGCGTCAG AAGCACCCAG GACTTCCATT  | 502  |
| TGCTTTGTCC CGGGGCTCCA CTGAACAAGT TGGCCTGCAC TGGTGTTTTG TTGTGGGGAG  | 562  |
| GAGGATGGGG AGTAGGACAT ACCAGCTTAG ATTTTAAGGT TTTTACTGTG AGGGATGTTT  | 622  |
| GGGAGATGTA AGAAATGTTT TTGCAGTTAA GGGTTAGTTT ACAATCAGCC ACATTCTAGG  | 682  |
| TAGGTAGGGG CCCACTTCAC CGTACTAACC AGGGAAGCTG TCCCTCATGT TGAATTTTCT  | 742  |
| CTAACTTCAA GGCCCATATC TGTGAAATGC TGGCATTTCG ACCTACCTCA CAGAGTGCAT  | 802  |
| TGTGAGGGTT AATGAAATAA TGTACATCTG GCCTTGAAAC CACCTTTTAT TACATGGGST  | 862  |
| CTAAAACTTG ACCCCCTTGA GGGTGCCTGT TCCCTCTCCC TCTCCCTGTT GGCTGGTGGG  | 922  |
| TTGGTAGTTT CTACAGTTGG GCAGCTGGTT AGGTAGAGGG AGTTGTCAAG TCTTGTCTGGC | 982  |
| CCAGCCAAAC CCGTGTCTGAC AACCTCTTGG TCGACCTTAG TACCTAAAAG GAAATCTCAC | 1042 |
| CCCATCC  | 1049 |

(2) INFORMATION FOR SEQ ID NO: 40:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

TTCTTCCACA TTCACCT

17

(2) INFORMATION FOR SEQ ID NO: 41:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

TCTTCCACAT TCACCTT

17

(2) INFORMATION FOR SEQ ID NO: 42:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CTTCCACATT CACCTTG

17

(2) INFORMATION FOR SEQ ID NO: 43:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

TTCCACATTC ACCTTGC

17

(2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

TCCACATTCA CCTTGGC

17

(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

CCACATTAC CTTGCCC

17

(2) INFORMATION FOR SEQ ID NO: 46:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

CACATTCAACC TTGCCCC

17

(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

ACATTCACTT TGCCCCA

17

(2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CATTCACTT GCCCCAC

17

(2) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

ATTACCTTG CCCACA

17

(2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

TTCACCTTGC CCCACAG

17

(2) INFORMATION FOR SEQ ID NO: 51:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

TCACCTTGCC CCACAGG

17

(2) INFORMATION FOR SEQ ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

CACCTTGCCC CACAGGG

17

(2) INFORMATION FOR SEQ ID NO: 53:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

ACCTTGCCCC ACAGGGC

17

(2) INFORMATION FOR SEQ ID NO: 54:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

CCTTGCCCCA CAGGGCA

17

(2) INFORMATION FOR SEQ ID NO: 55:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

CTTGCCCCAC AGGCGCAG

17

(2) INFORMATION FOR SEQ ID NO: 56:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

TTGCCCCACA GGGCAGT

17

(2) INFORMATION FOR SEQ ID NO: 57:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

TGCCCCACAG GGCAGTG

17

(2) INFORMATION FOR SEQ ID NO: 58:

00784674.021501  
10120.4494269

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

GCCCCACAGG GCAGTGA

17

(2) INFORMATION FOR SEQ ID NO: 59:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

CCCCACAGGG CAGTGAC

17

(2) INFORMATION FOR SEQ ID NO: 60:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

CCCACAGGGC AGTGACC

17

(2) INFORMATION FOR SEQ ID NO: 61:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

CCACAGGGCA GTGACCG

17

(2) INFORMATION FOR SEQ ID NO: 62:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

CACAGGGCAG TGACCGC

17

(2) INFORMATION FOR SEQ ID NO: 63:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

ACAGGGCAGT GACCGCA

17

(2) INFORMATION FOR SEQ ID NO: 64:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

CAGGGCAGTG ACCGCAG

17

(2) INFORMATION FOR SEQ ID NO: 65:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

AGGGCAGTGA CCGCAGA

17

(2) INFORMATION FOR SEQ ID NO: 66:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

GGGCAGTGAC CGCAGAC

17

(2) INFORMATION FOR SEQ ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

GGCAGTGACC GCAGACT

17

(2) INFORMATION FOR SEQ ID NO: 68:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

GCAGTGACCG CAGACTT

17

(2) INFORMATION FOR SEQ ID NO: 69:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

09784674.021504

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

CAGTGACCGC AGACTTC

17

(2) INFORMATION FOR SEQ ID NO: 70:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

AGTGACCGCA GACTTCT

17

(2) INFORMATION FOR SEQ ID NO: 71:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

GTGACCGCAG ACTTCTC

17

(2) INFORMATION FOR SEQ ID NO: 72:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

TGACCGCAGA CTTCTCC

17

(2) INFORMATION FOR SEQ ID NO: 73:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

GACCGCAGAC TTTCCT

17

(2) INFORMATION FOR SEQ ID NO: 74:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

ACCGCAGACT TCTCCTC

17

(2) INFORMATION FOR SEQ ID NO: 75:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs

105120.42948260

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

CCGCAGACTT CTCCTCA

17

(2) INFORMATION FOR SEQ ID NO: 76:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

CGCAGACTTC TCCTCAC

17

(2) INFORMATION FOR SEQ ID NO: 77:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

GCAGACTTCT CCTCACT

17

(2) INFORMATION FOR SEQ ID NO: 78:

05784634.021501

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

CAGACTTCTC CTCACTG

17

(2) INFORMATION FOR SEQ ID NO: 79:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

AGACTTCTCC TCAC TGG

17

(2) INFORMATION FOR SEQ ID NO: 80:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

GACTTCTCCT CACTGGA

17

(2) INFORMATION FOR SEQ ID NO: 81:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

ACTTCTCCTC ACTGGAC

17

(2) INFORMATION FOR SEQ ID NO: 82:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

CTTCTCCTCA CTGGACA

17

(2) INFORMATION FOR SEQ ID NO: 83:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

TTCTCCTCAC TGGACAG

17

(2) INFORMATION FOR SEQ ID NO: 84:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 17 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

TCTCCTCACT GGACAGA

17

(2) INFORMATION FOR SEQ ID NO: 85:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 17 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

CTCCTCACTG GACAGAT

17

(2) INFORMATION FOR SEQ ID NO: 86:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 17 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

TCCTCACTGG ACAGATG

17

(2) INFORMATION FOR SEQ ID NO: 87:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

CCTCACTGGA CAGATGC

17

(2) INFORMATION FOR SEQ ID NO: 88:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

CTCACTGGAC AGATGCA

17

(2) INFORMATION FOR SEQ ID NO: 89:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

09784674-021501

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

TCACTGGACA GATGCAC

17

(2) INFORMATION FOR SEQ ID NO: 90:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

CACTGGACAG ATGCACC

17

(2) INFORMATION FOR SEQ ID NO: 91:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

ACTGGACAGA TGCACCA

17

(2) INFORMATION FOR SEQ ID NO: 92:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

CTGGACAGAT GCACCAT

17

(2) INFORMATION FOR SEQ ID NO: 93:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

TGGACAGATG CACCATT

17

(2) INFORMATION FOR SEQ ID NO: 94:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

GGACAGATGC ACCATTG

17

(2) INFORMATION FOR SEQ ID NO: 95:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

GACAGATGCA CCATTCT

17

(2) INFORMATION FOR SEQ ID NO: 96:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

ACAGATGCAC CATTCTG

17

(2) INFORMATION FOR SEQ ID NO: 97:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

CAGATGCACC ATTCTGT

17

(2) INFORMATION FOR SEQ ID NO: 98:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

AGATGCACCA TTCTGTC

17

(2) INFORMATION FOR SEQ ID NO: 99:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

GATGCACCAT TCTGTCT

17

(2) INFORMATION FOR SEQ ID NO: 100:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

ATGCACCATT CTGTCTG

17

(2) INFORMATION FOR SEQ ID NO: 101:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

TGCACCATTC TGTCTGT

17

(2) INFORMATION FOR SEQ ID NO: 102:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

GCACCATTTCT GTCTGTT

17

(2) INFORMATION FOR SEQ ID NO: 103:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

097814674.021501

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

CACCATTCCTG TCTGTTT

17

(2) INFORMATION FOR SEQ ID NO: 104:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

ACCATTCCTGT CTGTTTT

17

(2) INFORMATION FOR SEQ ID NO: 105:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

CCATTCCTGTC TGTTTTG

17

(2) INFORMATION FOR SEQ ID NO: 106:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

CATTCTGTCT GTTTGG

17

(2) INFORMATION FOR SEQ ID NO: 107:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 17 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

ATTCTGTCTG TTTGGG

17

(2) INFORMATION FOR SEQ ID NO: 108:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 17 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

TTCTGTCTGT TTTGGG

17

(2) INFORMATION FOR SEQ ID NO: 109:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 17 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

TCTGTCTGTT TTGGGGG

17

(2) INFORMATION FOR SEQ ID NO: 110:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

CTGTCTGTTT TGGGGGA

17

(2) INFORMATION FOR SEQ ID NO: 111:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

TGTCTGTTTT GGGGGAT

17

(2) INFORMATION FOR SEQ ID NO: 112:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

GTCTGTTTGG GGGGATT

17

(2) INFORMATION FOR SEQ ID NO: 113:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

TCTGTTTGG GGGATTG

17

(2) INFORMATION FOR SEQ ID NO: 114:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

CTGTTTGGG GGATTGC

17

(2) INFORMATION FOR SEQ ID NO: 115:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

TGTTTGGGG GATTGCA

17

(2) INFORMATION FOR SEQ ID NO: 116:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

GTTTGGGGG ATTGCAA

17

(2) INFORMATION FOR SEQ ID NO: 117:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

TTTGGGGGA TTGCAAG

17

(2) INFORMATION FOR SEQ ID NO: 118:

0978446744.021501

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

TTTGGGGGAT TGCAAGT

17

(2) INFORMATION FOR SEQ ID NO: 119:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

TTGGGGGATT GCAAGTA

17

(2) INFORMATION FOR SEQ ID NO: 120:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

10971464-1

TGGGGGATTG CAAGTAA

17

(2) INFORMATION FOR SEQ ID NO: 121:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

GGGGGATTGC AAGTAA

17

(2) INFORMATION FOR SEQ ID NO: 122:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

GGGGATTGCA AGTAAAC

17

(2) INFORMATION FOR SEQ ID NO: 123:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

10971464-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

GGGATTGCAA GTAAACA

17

(2) INFORMATION FOR SEQ ID NO: 124:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

GGATTGCAAG TAAACAC

17

(2) INFORMATION FOR SEQ ID NO: 125:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

GATTGCAAGT AAACACA

17

(2) INFORMATION FOR SEQ ID NO: 126:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

ATTGCAAGTA AACACAG

17

(2) INFORMATION FOR SEQ ID NO: 127:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

TTGCAAGTAA ACACAGT

17

(2) INFORMATION FOR SEQ ID NO: 128:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

TGCAAGTAAA CACAGTT

17

(2) INFORMATION FOR SEQ ID NO: 129:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

GCAAGTAAAC ACAGTTG

17

(2) INFORMATION FOR SEQ ID NO: 130:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

CAAGTAAACA CAGTTGT

17

(2) INFORMATION FOR SEQ ID NO: 131:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

AAGTAAACAC AGTTGTG

17

(2) INFORMATION FOR SEQ ID NO: 132:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

AGTAAACACA GTTGTGT

17

(2) INFORMATION FOR SEQ ID NO: 133:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

GTAAACACAG TTGTGTC

17

(2) INFORMATION FOR SEQ ID NO: 134:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

TAAACACAGT TGTGTCA

17

(2) INFORMATION FOR SEQ ID NO: 135:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs

09784674.021501

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

AAACACAGTT GTGTCAA

17

(2) INFORMATION FOR SEQ ID NO: 136:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

AACACAGTTG TGTCAA

17

(2) INFORMATION FOR SEQ ID NO: 137:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

ACACAGTTGT GTCAAAA

17

(2) INFORMATION FOR SEQ ID NO: 138:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

CACAGTTGTG TCAAAAG

17

(2) INFORMATION FOR SEQ ID NO: 139:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

ACAGTTGTGT CAAAAGC

17

(2) INFORMATION FOR SEQ ID NO: 140:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

CAGTTGTGTC AAAAGCA

17

(2) INFORMATION FOR SEQ ID NO: 141:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

AGTTGTGTCA AAAGCAA

17

(2) INFORMATION FOR SEQ ID NO: 142:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

GTTGTGTCAA AAGCAAG

17

(2) INFORMATION FOR SEQ ID NO: 143:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

TTGTGTCAAA AGCAAGT

17

(2) INFORMATION FOR SEQ ID NO: 144:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

TGTGTCAAAA GCAAGT

17

(2) INFORMATION FOR SEQ ID NO: 145:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

GTACTGTCCA TTTATCAGGA

20

(2) INFORMATION FOR SEQ ID NO: 146:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

TACTGTCCAT TTATCAGGAT

20

(2) INFORMATION FOR SEQ ID NO: 147:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

ACTGTCCATT TATCAGGATG

20

(2) INFORMATION FOR SEQ ID NO: 148:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

CTGTCCATTT ATCAGGATGG

20

(2) INFORMATION FOR SEQ ID NO: 149:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

TGTCCATTTA TCAGGATGGA

20

(2) INFORMATION FOR SEQ ID NO: 150:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

GTCCATTAT CAGGATGGAG

20

(2) INFORMATION FOR SEQ ID NO: 151:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

TCCATTTATC AGGATGGAGT

20

(2) INFORMATION FOR SEQ ID NO: 152:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

CCATTTATCA GGATGGAGTT

20

(2) INFORMATION FOR SEQ ID NO: 153:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

CATTTATCAG GATGGAGTTC

20

(2) INFORMATION FOR SEQ ID NO: 154:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

ATTTATCAGG ATGGAGTTCA

20

(2) INFORMATION FOR SEQ ID NO: 155:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

TTTATCAGGA TGGAGTTCAT

20

(2) INFORMATION FOR SEQ ID NO: 156:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

TTATCAGGAT GGAGTTCATA

20

(2) INFORMATION FOR SEQ ID NO: 157:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

TATCAGGATG GAGTTCATAA

20

(2) INFORMATION FOR SEQ ID NO: 158:

09784674-021501

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

ATCAGGATGG AGTTCATAAC

20

(2) INFORMATION FOR SEQ ID NO: 159:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

TCAGGATGGA GTTCATAACC

20

(2) INFORMATION FOR SEQ ID NO: 160:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

09784674.021504

CAGGATGGAG TTCATAACCC

20

(2) INFORMATION FOR SEQ ID NO: 161:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

AGGATGGAGT TCATAACCCA

20

(2) INFORMATION FOR SEQ ID NO: 162:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

GGATGGAGTT CATAACCCAT

20

(2) INFORMATION FOR SEQ ID NO: 163:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

09764674-023504

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

GATGGAGTTC ATAACCCATC

20

(2) INFORMATION FOR SEQ ID NO: 164:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

ATGGAGTTCA TAACCCATCC

20

(2) INFORMATION FOR SEQ ID NO: 165:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

TGGAGTTCAT AACCCATCCC

20

(2) INFORMATION FOR SEQ ID NO: 166:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

GGAGTTCATA ACCCATCCCA

20

(2) INFORMATION FOR SEQ ID NO: 167:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

GAGTTCATAA CCCATCCCAA

20

(2) INFORMATION FOR SEQ ID NO: 168:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

AGTTCATAAC CCATCCCAAA

20

(2) INFORMATION FOR SEQ ID NO: 169:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

09734574-02500  
105520-12502620

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

G TTCATAACC CATCCAAAG

20

(2) INFORMATION FOR SEQ ID NO: 170:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

TTCATAACCC ATCCCAAAGG

20

(2) INFORMATION FOR SEQ ID NO: 171:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

TCATAACCCA TCCCAAAGGA

20

(2) INFORMATION FOR SEQ ID NO: 172:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

CATAACCCAT CCCAAAGGAA

20

(2) INFORMATION FOR SEQ ID NO: 173:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

ATAACCCATC CCAAAGGAAT

20

(2) INFORMATION FOR SEQ ID NO: 174:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

TAACCCATCC CAAAGGAATG

20

(2) INFORMATION FOR SEQ ID NO: 175:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

AACCCATCCC AAAGGAATGG

20

(2) INFORMATION FOR SEQ ID NO: 176:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

ACCCATCCCA AAGGAATGGA

20

(2) INFORMATION FOR SEQ ID NO: 177:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

CCCATCCCAA AGGAATGGAG

20

(2) INFORMATION FOR SEQ ID NO: 178:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

CCATCCCAAA GGAATGGAGG

20

(2) INFORMATION FOR SEQ ID NO: 179:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

CATCCCAAAG GAATGGAGGT

20

(2) INFORMATION FOR SEQ ID NO: 180:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

00734674-001501

ATCCCAAAGG AATGGAGGTT

20

(2) INFORMATION FOR SEQ ID NO: 181:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

TCCCAAAGGA ATGAGGTTTC

20

(2) INFORMATION FOR SEQ ID NO: 182:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

CCCAAAGGAA TGGAGGTTCT

20

(2) INFORMATION FOR SEQ ID NO: 183:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

CCAAAGGAAT GGAGTTCCTT

20

(2) INFORMATION FOR SEQ ID NO: 184:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

CAAAGGAATG GAGGTTCTTT

20

(2) INFORMATION FOR SEQ ID NO: 185:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

AAAGGAATGG AGGTTCTTTC

20

(2) INFORMATION FOR SEQ ID NO: 186:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

09704674-021504

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

AAGGAATGGA GGTCTTTCT

20

(2) INFORMATION FOR SEQ ID NO: 187:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

AGGAATGGAG GTCTTTCTG

20

(2) INFORMATION FOR SEQ ID NO: 188:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

GGAATGGAGG TTCTTTCTGA

20

(2) INFORMATION FOR SEQ ID NO: 189:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

GAATGGAGGT TCTTCTGAT

20

(2) INFORMATION FOR SEQ ID NO: 190:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

AATGGAGGTT CTTTCTGATG

20

(2) INFORMATION FOR SEQ ID NO: 191:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

ATGGAGGTTC TTCTGATGT

20

(2) INFORMATION FOR SEQ ID NO: 192:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

TGGAGGTTCT TTCTGATGTT

20

(2) INFORMATION FOR SEQ ID NO: 193:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

GGAGGTTCTT TCTGATGTTT

20

(2) INFORMATION FOR SEQ ID NO: 194:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

GAGGTTCTTT CTGATGTTT

20

(2) INFORMATION FOR SEQ ID NO: 195:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

AGGTTCTTTC TGATGTTTTT

20

(2) INFORMATION FOR SEQ ID NO: 196:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

GGTCTTTTCT GATGTTTTTT

20

(2) INFORMATION FOR SEQ ID NO: 197:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

GTTCTTTCTG ATGTTTTTTG

20

(2) INFORMATION FOR SEQ ID NO: 198:

10971464-1

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

TTCTTTCTGA GTTTTTTGT

20

(2) INFORMATION FOR SEQ ID NO: 199:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

TCCTTCTGAT GTTTTTTGTG

20

(2) INFORMATION FOR SEQ ID NO: 200:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

CTTCTGATG TTTTGTCT

20

(2) INFORMATION FOR SEQ ID NO: 201:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

TTTCTGATG TTTTGTCTG

20

(2) INFORMATION FOR SEQ ID NO: 202:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

TTTCTGATG TTTTGTCTG

20

(2) INFORMATION FOR SEQ ID NO: 203:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

TCTGATGTTT TTTGCTCGGT

20

(2) INFORMATION FOR SEQ ID NO: 204:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

CTGATGTTTT TTGCTCGGTG

20

(2) INFORMATION FOR SEQ ID NO: 205:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

TGATGTTTTT TGCTCGGTGT

20

(2) INFORMATION FOR SEQ ID NO: 206:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

GATGTTTTTT GTCTGGTGTG

20

(2) INFORMATION FOR SEQ ID NO: 207:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

ATGTTTTTTG TCTGGTGTGG

20

(2) INFORMATION FOR SEQ ID NO: 208:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

TGTTTTTTGT CTGGTGTGGT

20

(2) INFORMATION FOR SEQ ID NO: 209:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

GTTTTTTGTC TGGTGTGGTA

20

(2) INFORMATION FOR SEQ ID NO: 210:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

TTTTTTGTCT GGTGTGGTAA

20

(2) INFORMATION FOR SEQ ID NO: 211:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

TTTTTGTCTG GTGTGGTAAG

20

(2) INFORMATION FOR SEQ ID NO: 212:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

TTTGTCTGG TGTGTAAGT

20

(2) INFORMATION FOR SEQ ID NO: 213:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

TTTGTCTGGT GTGTAAGTC

20

(2) INFORMATION FOR SEQ ID NO: 214:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

TTGTCTGGTG TGGTAAGTCC

20

(2) INFORMATION FOR SEQ ID NO: 215:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs

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(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

TGTCCTGGTGT GGTAAGTCCC

20

(2) INFORMATION FOR SEQ ID NO: 216:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

GTCTGGTGTG GTAAGTCCCC

20

(2) INFORMATION FOR SEQ ID NO: 217:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

TCTGGTGTGG TAAGTCCCCA

20

(2) INFORMATION FOR SEQ ID NO: 218:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

CTGGTGTGGT AAGTCCCCAC

20

(2) INFORMATION FOR SEQ ID NO: 219:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

TGGTGTGGTA AGTCCCCACC

20

(2) INFORMATION FOR SEQ ID NO: 220:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

09784674.021501

GGTGTGGTAA GTCCCCACCT

20

(2) INFORMATION FOR SEQ ID NO: 221:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

GTGTGGTAAG TCCCCACCTC

20

(2) INFORMATION FOR SEQ ID NO: 222:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

TGTGGTAAGT CCCCACCTCA

20

(2) INFORMATION FOR SEQ ID NO: 223:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

GTGGTAAGTC CCCACCTCAA

20

(2) INFORMATION FOR SEQ ID NO: 224:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

TGGTAAGTCC CCACCTCAAC

20

(2) INFORMATION FOR SEQ ID NO: 225:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

GGTAAGTCCC CACCTCAACA

20

(2) INFORMATION FOR SEQ ID NO: 226:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

GTAAGTCCCC ACCTCAACAG

20

(2) INFORMATION FOR SEQ ID NO: 227:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

TAAGTCCCCA CCTCAACAGA

20

(2) INFORMATION FOR SEQ ID NO: 228:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

AAGTCCCCAC CTCAACAGAT

20

(2) INFORMATION FOR SEQ ID NO: 229:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

AGTCCCCACC TCAACAGATG

20

(2) INFORMATION FOR SEQ ID NO: 230:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

GTCCTCCACCT CAACAGATGT

20

(2) INFORMATION FOR SEQ ID NO: 231:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

TCCCCACCTC AACAGATGTT

20

(2) INFORMATION FOR SEQ ID NO: 232:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

CCCCACCTCA ACAGATGTTG

20

(2) INFORMATION FOR SEQ ID NO: 233:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

CCCACCTCAA CAGATGTTGT

20

(2) INFORMATION FOR SEQ ID NO: 234:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

CCACCTCAAC AGATGTTGTC

20

(2) INFORMATION FOR SEQ ID NO: 235:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs

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(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

CACCTCAACA GATGTTGTCT

20

(2) INFORMATION FOR SEQ ID NO: 236:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

ACCTCAACAG ATGTTGCTC

20

(2) INFORMATION FOR SEQ ID NO: 237:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

CCTCAACAGA TGTTGTCTCA

20

(2) INFORMATION FOR SEQ ID NO: 238:

09784674.021501

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

CTCAACAGAT GTTGCTCAG

20

(2) INFORMATION FOR SEQ ID NO: 239:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

TCAACAGATG TTGTCTCAGC

20

(2) INFORMATION FOR SEQ ID NO: 240:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

CAACAGATGT TGTCTCAGCT

20

(2) INFORMATION FOR SEQ ID NO: 241:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

AACAGATGTT GTCTCAGCTC

20

(2) INFORMATION FOR SEQ ID NO: 242:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

ACAGATGTTG TCTCAGCTCC

20

(2) INFORMATION FOR SEQ ID NO: 243:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

CAGATGTTGT CTCAGCTCCT

20

(2) INFORMATION FOR SEQ ID NO: 244:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

AGATGTTGTC TCAGCTCCTC

20

(2) INFORMATION FOR SEQ ID NO: 245:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

GATGTTGTCT CAGCTCCTCT

20

(2) INFORMATION FOR SEQ ID NO: 246:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

ATGTTGTCTC AGCTCCTCTA

20

(2) INFORMATION FOR SEQ ID NO: 247:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

TGTTGTCTCA GTCCTCTAT

20

(2) INFORMATION FOR SEQ ID NO: 248:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

GTTGTCTCAG CTCCTCTATT

20

(2) INFORMATION FOR SEQ ID NO: 249:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

TTGTCTCAGC TCCTCTATTT

20

(2) INFORMATION FOR SEQ ID NO: 250:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

TGTCTCAGCT CCTCTATTTT

20

(2) INFORMATION FOR SEQ ID NO: 251:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

GTCTCAGCTC CTCTATTTT

20

(2) INFORMATION FOR SEQ ID NO: 252:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

TCTCAGCTCC TCTATTTTGG

20

(2) INFORMATION FOR SEQ ID NO: 253:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

CTCAGCTCCT CTATTTTGTG

20

(2) INFORMATION FOR SEQ ID NO: 254:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

TCAGCTCCTC TATTTTGTG

20

(2) INFORMATION FOR SEQ ID NO: 255:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs

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(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

CAGCTCCTCT ATTTTGTTC

20

(2) INFORMATION FOR SEQ ID NO: 256:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

AGCTCCTCTA TTTTGTCT

20

(2) INFORMATION FOR SEQ ID NO: 257:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

GCTCCTCTAT TTTTGTCTA

20

(2) INFORMATION FOR SEQ ID NO: 258:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

CTCCTCTATT TTTGTTCTAT

20

(2) INFORMATION FOR SEQ ID NO: 259:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

TCCTCTATTT TGTGTTCTATG

20

(2) INFORMATION FOR SEQ ID NO: 260:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

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CCTCTATTTT GTTCTATGCT

20

(2) INFORMATION FOR SEQ ID NO: 261:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

CTCTATTTT GTTCTATGCT

20

(2) INFORMATION FOR SEQ ID NO: 262:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

TCTATTTTGT TTCTATGCTG

20

(2) INFORMATION FOR SEQ ID NO: 263:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

CTATTTTGT TCTATGCTGC

20

(2) INFORMATION FOR SEQ ID NO: 264:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:

TATTTTGTCT CTATGCTGCC

20

(2) INFORMATION FOR SEQ ID NO: 265:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:

ATTTTGTTC TATGCTGCC

20

(2) INFORMATION FOR SEQ ID NO: 266:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

TTTTGTCTCT ATGCTGCCCT

20

(2) INFORMATION FOR SEQ ID NO: 267:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

TTTTGTCTTA TGCTGCCCTA

20

(2) INFORMATION FOR SEQ ID NO: 268:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

TTTGTCTCTAT GCTGCCCTAT

20

(2) INFORMATION FOR SEQ ID NO: 269:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

TTGTTCTATG CTGCCCTATT

20

(2) INFORMATION FOR SEQ ID NO: 270:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:

TGTTCTATGC TGCCCTATTT

20

(2) INFORMATION FOR SEQ ID NO: 271:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

GTTCTATGCT GCCCTATTTT

20

(2) INFORMATION FOR SEQ ID NO: 272:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:

TTCTATGCTG CCCTATTCTC

20

(2) INFORMATION FOR SEQ ID NO: 273:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

TCTATGCTGC CCTATTCTA

20

(2) INFORMATION FOR SEQ ID NO: 274:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

CTATGCTGCC CTATTCTAA

20

(2) INFORMATION FOR SEQ ID NO: 275:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs

09784674-021503

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:

TATGCTGCCC TATTCTAAG

20

(2) INFORMATION FOR SEQ ID NO: 276:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:

ATGCTGCCCT ATTTCTAAGT

20

(2) INFORMATION FOR SEQ ID NO: 277:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:

TGCTGCCCTA TTTCTAAGTC

20

(2) INFORMATION FOR SEQ ID NO: 278:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
  
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:

GCTGCCCTAT TTCTAAGTCA

20

(2) INFORMATION FOR SEQ ID NO: 279:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
  
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:

CTGCCCTATT TCTAAGTCAG

20

(2) INFORMATION FOR SEQ ID NO: 280:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
  
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:

TGCCCTATTT CTAAGTCAGA

20

(2) INFORMATION FOR SEQ ID NO: 281:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:

GCCCTATTTC TAAGTCAGAT

20

(2) INFORMATION FOR SEQ ID NO: 282:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:

CCCTATTTC T AAGTCAGATC

20

(2) INFORMATION FOR SEQ ID NO: 283:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

09784674.021501

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

CCTATTCTTA AGTCAGATCC

20

(2) INFORMATION FOR SEQ ID NO: 284:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

CTATTCTTAA GTCAGATCCT

20

(2) INFORMATION FOR SEQ ID NO: 285:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

TATTCTAAG TCAGATCCTA

20

(2) INFORMATION FOR SEQ ID NO: 286:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

ATTCTAAGT CAGATCCTAC

20

(2) INFORMATION FOR SEQ ID NO: 287:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:

TTTCTAAGTC AGATCCTACA

20

(2) INFORMATION FOR SEQ ID NO: 288:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:

TTCTAAGTCA GATCCTACAT

20

(2) INFORMATION FOR SEQ ID NO: 289:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:

TCTAAGTCAG ATCCTACATA

20

(2) INFORMATION FOR SEQ ID NO: 290:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:

CTAAGTCAGA TCCTACATAC

20

(2) INFORMATION FOR SEQ ID NO: 291:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:

TAAGTCAGAT CCTACATACA

20

(2) INFORMATION FOR SEQ ID NO: 292:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:

AAGTCAGATC CTACATACAA

20

(2) INFORMATION FOR SEQ ID NO: 293:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:

AGTCAGATCC TACATACAAA

20

(2) INFORMATION FOR SEQ ID NO: 294:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:

GTCAGATCCT ACATACAAAT

20

(2) INFORMATION FOR SEQ ID NO: 295:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:

TCAGATCCTA CATACAAATC

20

(2) INFORMATION FOR SEQ ID NO: 296:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:

CAGATCCTAC ATACAAATCA

20

(2) INFORMATION FOR SEQ ID NO: 297:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:

AGATCCTACA TACAAATCAT

20

(2) INFORMATION FOR SEQ ID NO: 298:

10971464.021501

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:

GATCCTACAT ACAAATCATC

20

(2) INFORMATION FOR SEQ ID NO: 299:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:299:

ATCCTACATA CAAATCATCC

20

(2) INFORMATION FOR SEQ ID NO: 300:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:

109784674.021501

TCCTACATAC AAATCATCCA

20

(2) INFORMATION FOR SEQ ID NO: 301:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:

CCTACATACA AATCATCCAT

20

(2) INFORMATION FOR SEQ ID NO: 302:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:

CTACATACAA ATCATCCATG

20

(2) INFORMATION FOR SEQ ID NO: 303:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

10971464-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:

TACATACAAA TCATCCATGT

20

(2) INFORMATION FOR SEQ ID NO: 304:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:

ACATACAAAT CATCCATGTA

20

(2) INFORMATION FOR SEQ ID NO: 305:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:

CATACAAATC ATCCATGTAT

20

(2) INFORMATION FOR SEQ ID NO: 306:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:

ATACAAATCA TCCATGTATT

20

(2) INFORMATION FOR SEQ ID NO: 307:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:

TACAAATCAT CCATGTATTG

20

(2) INFORMATION FOR SEQ ID NO: 308:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:308:

ACAAATCATC CATGTATTGA

20

(2) INFORMATION FOR SEQ ID NO: 309:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

00784674.021501

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:

CAAATCATCC ATGTATTGAT

20

(2) INFORMATION FOR SEQ ID NO: 310:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:

AAATCATCCA TGTATTGATA

20

(2) INFORMATION FOR SEQ ID NO: 311:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:

AATCATCCAT GTATTGATAG

20

(2) INFORMATION FOR SEQ ID NO: 312:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:

ATCATCCATG TATTGATAGA

20

(2) INFORMATION FOR SEQ ID NO: 313:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:

TCATCCATGT ATTGATAGAT

20

(2) INFORMATION FOR SEQ ID NO: 314:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:

CATCCATGTA TTGATAGATA

20

(2) INFORMATION FOR SEQ ID NO: 315:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs

09784674-021501

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:

ATCCATGTAT TGATAGATAA

20

(2) INFORMATION FOR SEQ ID NO: 316:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:

TCCATGTATT GATAGATAAC

20

(2) INFORMATION FOR SEQ ID NO: 317:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:

CCATGTATTG ATAGATAACT

20

(2) INFORMATION FOR SEQ ID NO: 318:

10971464-1

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:

CATGTATTGA TAGATAACTA

20

(2) INFORMATION FOR SEQ ID NO: 319:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:

ATGTATTGAT AGATAACTAT

20

(2) INFORMATION FOR SEQ ID NO: 320:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:

09734674-021504

TGTATTGATA GATAACTATG

20

(2) INFORMATION FOR SEQ ID NO: 321:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321:

GTATTGATAG ATAACATGTC

20

(2) INFORMATION FOR SEQ ID NO: 322:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:322:

TATTGATAGA TAACATGTC

20

(2) INFORMATION FOR SEQ ID NO: 323:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

10971464-1-021504

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:323:

ATTGATAGAT AACTATGTCT

20

(2) INFORMATION FOR SEQ ID NO: 324:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:324:

TTGATAGATA ACTATGTCTG

20

(2) INFORMATION FOR SEQ ID NO: 325:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:325:

TGATAGATAA CTATGTCTGG

20

(2) INFORMATION FOR SEQ ID NO: 326:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:326:

GATAGATAAC TATGTCTGGA

20

(2) INFORMATION FOR SEQ ID NO: 327:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:327:

ATAGATAACT ATGTCTGGAT

20

(2) INFORMATION FOR SEQ ID NO: 328:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:

TAGATAACTA TGTCTGGATT

20

(2) INFORMATION FOR SEQ ID NO: 329:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:329:

AGATAACTAT GTCTGGATTT

20

(2) INFORMATION FOR SEQ ID NO: 330:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:

GATAACTATG TCTGGATTTT

20

(2) INFORMATION FOR SEQ ID NO: 331:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:

ATAACTATGT CTGGATTTTG

20

(2) INFORMATION FOR SEQ ID NO: 332:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

1057420.12497460

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:332:

TAACTATGTC TGGATTTTGT

20

(2) INFORMATION FOR SEQ ID NO: 333:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:

AACTATGTCT GGATTTTGT

20

(2) INFORMATION FOR SEQ ID NO: 334:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:334:

ACTATGTCTG GATTTTGT

20

(2) INFORMATION FOR SEQ ID NO: 335:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:335:

CTATGTCTGG ATTTGTTTT

20

(2) INFORMATION FOR SEQ ID NO: 336:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:336:

TATGTCTGGA TTTGTTTT

20

(2) INFORMATION FOR SEQ ID NO: 337:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:337:

ATGTCTGGAT TTTGTTTT

20

(2) INFORMATION FOR SEQ ID NO: 338:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:338:

TGCTCTGGATT TTGTTTTTTA

20

(2) INFORMATION FOR SEQ ID NO: 339:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:339:

GTCTGGATTT TGTTTTTTAA

20

(2) INFORMATION FOR SEQ ID NO: 340:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:340:

00784674-021571

TCTGGATTTT GTTTTTTAAA

20

(2) INFORMATION FOR SEQ ID NO: 341:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:341:

CTGGATTTTG TTTTTTAAA

20

(2) INFORMATION FOR SEQ ID NO: 342:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:342:

TGGATTTTGT TTTTAAAAG

20

(2) INFORMATION FOR SEQ ID NO: 343:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:343:

GGATTTTGTT TTTTAAAGG

20

(2) INFORMATION FOR SEQ ID NO: 344:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:344:

GATTTTGTTT TTTTAAAGGC

20

(2) INFORMATION FOR SEQ ID NO: 345:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:345:

ATTTTGTTTT TTAAAGGCT

20

(2) INFORMATION FOR SEQ ID NO: 346:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:346:

TTTGTTTTT TAAAGGCTC

20

(2) INFORMATION FOR SEQ ID NO: 347:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:347:

TTTGTTTTT AAAAGGCTCT

20

(2) INFORMATION FOR SEQ ID NO: 348:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:348:

TTGTTTTTTA AAAGGCTCTA

20

(2) INFORMATION FOR SEQ ID NO: 349:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:349:

TGTTTTTTTAA AAGGCTCTAA

20

(2) INFORMATION FOR SEQ ID NO: 350:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:350:

GTTTTTTTAAA AGGCTCTAAG

20

(2) INFORMATION FOR SEQ ID NO: 351:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:351:

TTTTTTTAAAA GGCTCTAAGA

20

(2) INFORMATION FOR SEQ ID NO: 352:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:352:

TTTTTAAAG GCTCTAAGAT

20

(2) INFORMATION FOR SEQ ID NO: 353:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:353:

TTTTAAAGG CTCTAAGATT

20

(2) INFORMATION FOR SEQ ID NO: 354:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:354:

TTTAAAGGC TCTAAGATT

20

(2) INFORMATION FOR SEQ ID NO: 355:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:355:

TTAAAAGGCT CTAAGATTTT

20

(2) INFORMATION FOR SEQ ID NO: 356:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:356:

TAAAAGGCTC TAAGATTTT

20

(2) INFORMATION FOR SEQ ID NO: 357:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:357:

AAAAGGCTCT AAGATTTTGT

20

(2) INFORMATION FOR SEQ ID NO: 358:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:358:

AAAGGCTCTA AGATTTTGTG

20

(2) INFORMATION FOR SEQ ID NO: 359:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:359:

AAGGCTCTAA GATTTTGTG

20

(2) INFORMATION FOR SEQ ID NO: 360:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:360:

09734674-021401

AGGCTCTAAG ATTTTGTCA

20

(2) INFORMATION FOR SEQ ID NO: 361:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:361:

GGCTCTAAGA TTTTGTGCAT

20

(2) INFORMATION FOR SEQ ID NO: 362:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:362:

GCTCTAAGAT TTTTGTGCATG

20

(2) INFORMATION FOR SEQ ID NO: 363:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

09724674.121504

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:363:

CTCTAAGATT TTTGTCATGC

20

(2) INFORMATION FOR SEQ ID NO: 364:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:364:

TCTAAGATTT TTGTCATGCT

20

(2) INFORMATION FOR SEQ ID NO: 365:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:365:

CTAAGATTTT TGTCATGCTA

20

(2) INFORMATION FOR SEQ ID NO: 366:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:366:

TAAGATTTT GTCATGCTAC

20

(2) INFORMATION FOR SEQ ID NO: 367:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:367:

AAGATTTTGT TCATGCTACT

20

(2) INFORMATION FOR SEQ ID NO: 368:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:368:

AGATTTTGT CATGCTACTT

20

(2) INFORMATION FOR SEQ ID NO: 369:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:369:

GATTTTGTGTC ATGCTACTTT

20

(2) INFORMATION FOR SEQ ID NO: 370:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:370:

ATTTTGTGCA TGCTACTTTG

20

(2) INFORMATION FOR SEQ ID NO: 371:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:371:

TTTTTGCAT GCTACTTTGG

20

(2) INFORMATION FOR SEQ ID NO: 372:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:372:

TTTTGTCATG CTA CTTTGGGA

20

(2) INFORMATION FOR SEQ ID NO: 373:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:373:

TTTGTCATGC TACTTTGGAA

20

(2) INFORMATION FOR SEQ ID NO: 374:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:374:

TTGTCATGCT ACTTTGGAAT

20

(2) INFORMATION FOR SEQ ID NO: 375:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs

10571674.021501

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:375:

TGTCATGCTA CTTTGAATA

20

(2) INFORMATION FOR SEQ ID NO: 376:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:376:

GTCATGCTAC TTTGAATAT

20

(2) INFORMATION FOR SEQ ID NO: 377:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:377:

TCATGCTACT TTGAATATT

20

(2) INFORMATION FOR SEQ ID NO: 378:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:378:

CATGCTACTT TGAATATTG

20

(2) INFORMATION FOR SEQ ID NO: 379:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:379:

ATGCTACTTT GGAATATTGC

20

(2) INFORMATION FOR SEQ ID NO: 380:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:380:

09784574.021501

TGCTACTTTG GAATATTGCT

20

(2) INFORMATION FOR SEQ ID NO: 381:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:381:

GCTACTTTGG AATATTGCTG

20

(2) INFORMATION FOR SEQ ID NO: 382:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:382:

CTACTTTGGA ATATTGCTGG

20

(2) INFORMATION FOR SEQ ID NO: 383:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:383:

TACTTTGGAA TATTGCTGGT

20

(2) INFORMATION FOR SEQ ID NO: 384:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:384:

ACTTTGGAAT ATTGCTGGTG

20

(2) INFORMATION FOR SEQ ID NO: 385:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:385:

CTTTGGAATA TTGCTGGTGA

20

(2) INFORMATION FOR SEQ ID NO: 386:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:386:

TTTGAATAT TGCTGGTGAT

20

(2) INFORMATION FOR SEQ ID NO: 387:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387:

TTGGAATATT GCTGGTGATC

20

(2) INFORMATION FOR SEQ ID NO: 388:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:388:

TGGAATATTG CTGGTGATCC

20

(2) INFORMATION FOR SEQ ID NO: 389:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:389:

GGAATATTGC TGGTGATCCT

20

(2) INFORMATION FOR SEQ ID NO: 390:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:390:

GAATATTGCT GGTGATCCTT

20

(2) INFORMATION FOR SEQ ID NO: 391:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:391:

AATATTGCTG GTGATCCTTT

20

(2) INFORMATION FOR SEQ ID NO: 392:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

09704674-021501

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:392:

ATATTGCTGG TGATCCTTTC

20

(2) INFORMATION FOR SEQ ID NO: 393:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:393:

TATTGCTGGT GATCCTTTCC

20

(2) INFORMATION FOR SEQ ID NO: 394:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:394:

ATTGCTGGTG ATCCTTTCCA

20

(2) INFORMATION FOR SEQ ID NO: 395:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs

10971464-1021501

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:395:

TTGCTGGTGA TCCTTCCAT

20

(2) INFORMATION FOR SEQ ID NO: 396:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:396:

TGCTGGTGAT CTTTCCATC

20

(2) INFORMATION FOR SEQ ID NO: 397:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:397:

GCTGGTGATC CTTTCCATC

20

(2) INFORMATION FOR SEQ ID NO: 398:

09784674-021501

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:398:

CTGGTGATCC TTTCATCCC

20

(2) INFORMATION FOR SEQ ID NO: 399:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:399:

TGGTGATCCT TTCCATCCCT

20

(2) INFORMATION FOR SEQ ID NO: 400:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:400:

GGTGATCCTT TCCATCCCTG

20

(2) INFORMATION FOR SEQ ID NO: 401:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:401:

GTGATCCTTT CCATCCCTGT

20

(2) INFORMATION FOR SEQ ID NO: 402:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:402:

TGATCCTTTC CATCCCTGTG

20

(2) INFORMATION FOR SEQ ID NO: 403:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

09784674-021501

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:403:

GATCCTTTCC ATCCCTGTGG

20

(2) INFORMATION FOR SEQ ID NO: 404:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:404:

ATCCTTTCCA TCCTGTGGA

20

(2) INFORMATION FOR SEQ ID NO: 405:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:405:

TCCTTTCCAT CCCTGTGGAA

20

(2) INFORMATION FOR SEQ ID NO: 406:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:406:

CCTTTCCATC CCTGTGGAAG

20

(2) INFORMATION FOR SEQ ID NO: 407:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:407:

CTTTCCATCC CTGTGGAAGC

20

(2) INFORMATION FOR SEQ ID NO: 408:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:408:

TTTCCATCCC TGTGGAAGCA

20

(2) INFORMATION FOR SEQ ID NO: 409:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:409:

TTCCATCCCT GTGGAAGCAC

20

(2) INFORMATION FOR SEQ ID NO: 410:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:410:

TCCATCCCTG TGAAGCACCA

20

(2) INFORMATION FOR SEQ ID NO: 411:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:411:

CCATCCCTGT GGAAGCACAT

20

(2) INFORMATION FOR SEQ ID NO: 412:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:412:

CATCCCTGTG GAAGCACATT

20

(2) INFORMATION FOR SEQ ID NO: 413:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:413:

ATCCCTGTGG AAGCACATTG

20

(2) INFORMATION FOR SEQ ID NO: 414:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:414:

TCCCTGTGGA AGCACATTGT

20

(2) INFORMATION FOR SEQ ID NO: 415:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:415:

CCCTGTGGAA GCACATTGTA

20

(2) INFORMATION FOR SEQ ID NO: 416:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:416:

CCTGTGGAAG CACATTGTAC

20

(2) INFORMATION FOR SEQ ID NO: 417:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:417:

CTGTGGAAGC ACATTGTACT

20

(2) INFORMATION FOR SEQ ID NO: 418:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:418:

TGTGGAAGCA CATTGTACTG

20

(2) INFORMATION FOR SEQ ID NO: 419:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:419:

GTGGAAGCAC ATTGTACTGA

20

(2) INFORMATION FOR SEQ ID NO: 420:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:420:

TGGAAGCACA TTGTACTGAT

20

(2) INFORMATION FOR SEQ ID NO: 421:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:421:

GGAAGCACAT TGTACTGATA

20

(2) INFORMATION FOR SEQ ID NO: 422:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:422:

GAAGCACATT GTACTGATAT

20

(2) INFORMATION FOR SEQ ID NO: 423:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:423:

AAGCACATTG TACTGATATC

20

(2) INFORMATION FOR SEQ ID NO: 424:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:424:

AGCACATTGT ACTGATATCT

20

(2) INFORMATION FOR SEQ ID NO: 425:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:425:

GCACATTGTA CTGATATCTA

20

(2) INFORMATION FOR SEQ ID NO: 426:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:426:

CACATTGTAC TGATATCTAA

20

(2) INFORMATION FOR SEQ ID NO: 427:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:427:

ACATTGTACT GATATCTAAT

20

(2) INFORMATION FOR SEQ ID NO: 428:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:428:

CATTGTACTG ATATCTAATC

20

(2) INFORMATION FOR SEQ ID NO: 429:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

105120.429126

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:429:

ATTGTACTGA TATCTAATCC

20

(2) INFORMATION FOR SEQ ID NO: 430:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:430:

TTGTACTGAT ATCTAATCCC

20

(2) INFORMATION FOR SEQ ID NO: 431:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:431:

TGTACTGATA TCTAATCCCT

20

(2) INFORMATION FOR SEQ ID NO: 432:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:432:

GTACTGATAT CTAATCCCTG

20

(2) INFORMATION FOR SEQ ID NO: 433:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:433:

TACTGATATC TAATCCCTGG

20

(2) INFORMATION FOR SEQ ID NO: 434:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:434:

ACTGATATCT AATCCCTGGT

20

(2) INFORMATION FOR SEQ ID NO: 435:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:435:

CTGATATCTA ATCCCTGGTG

20

(2) INFORMATION FOR SEQ ID NO: 436:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:436:

TGATATCTAA TCCCTGGTGT

20

(2) INFORMATION FOR SEQ ID NO: 437:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:437:

GATATCTAAT CCCTGGTGTGTC

20

(2) INFORMATION FOR SEQ ID NO: 438:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:438:

ATATCTAATC CCTGGTGTCT

20

(2) INFORMATION FOR SEQ ID NO: 439:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:439:

TATCTAATCC CTGGTGTCTC

20

(2) INFORMATION FOR SEQ ID NO: 440:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:440:

ATCTAATCCC TGGTGCTCA

20

(2) INFORMATION FOR SEQ ID NO: 441:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:441:

TCTAATCCCT GGTGTCTCAT

20

(2) INFORMATION FOR SEQ ID NO: 442:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:442:

CTAATCCCTG GTGTCTCATT

20

(2) INFORMATION FOR SEQ ID NO: 443:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:443:

TAATCCCTGG TGTCTCATTG

20

(2) INFORMATION FOR SEQ ID NO: 444:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:444:

AATCCCTGGT GTCTCATTGT

20

(2) INFORMATION FOR SEQ ID NO: 445:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:445:

ATCCCTGGTG TCTCATTGTT

20

(2) INFORMATION FOR SEQ ID NO: 446:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:446:

TCCCTGGTGT CTCATTGTTT

20

(2) INFORMATION FOR SEQ ID NO: 447:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:447:

CCCTGGTGTC TCATTGTTTA

20

(2) INFORMATION FOR SEQ ID NO: 448:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:448:

CCTGGTGTCT CATTGTTTAT

20

(2) INFORMATION FOR SEQ ID NO: 449:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:449:

CTGGTGTCTC ATTGTTTATA

20

(2) INFORMATION FOR SEQ ID NO: 450:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:450:

TGGTGTCTCA TTGTTTATAC

20

(2) INFORMATION FOR SEQ ID NO: 451:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:451:

GGTGTCTCAT TGTTTATACT

20

(2) INFORMATION FOR SEQ ID NO: 452:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:452:

GTGTCCTCATT GTTTATACTA

20

(2) INFORMATION FOR SEQ ID NO: 453:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:453:

TGTCTCATTG TTTATACTAG

20

(2) INFORMATION FOR SEQ ID NO: 454:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:454:

GTCTCATTGT TTATACTAGG

20

(2) INFORMATION FOR SEQ ID NO: 455:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:455:

TCTCATTGTT TATACTAGGT

20

(2) INFORMATION FOR SEQ ID NO: 456:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:456:

CTCATTGTTT ATACTAGGTA

20

(2) INFORMATION FOR SEQ ID NO: 457:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:457:

TCATTGTTTA TACTAGGTAT

20

(2) INFORMATION FOR SEQ ID NO: 458:

097844674-021501

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:458:

CATTGTTTAT ACTAGGTATG

20

(2) INFORMATION FOR SEQ ID NO: 459:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:459:

ATTGTTTATA CTAGGTATGG

20

(2) INFORMATION FOR SEQ ID NO: 460:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:460:

10971454-1

TTGTTTATAC TAGGTATGGT

20

(2) INFORMATION FOR SEQ ID NO: 461:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:461:

TGTTTATACT AGGTATGGTA

20

(2) INFORMATION FOR SEQ ID NO: 462:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:462:

GTTTATACTA GGTATGGTAA

20

(2) INFORMATION FOR SEQ ID NO: 463:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:463:

TTTATACTAG GTATGGTAAA

20

(2) INFORMATION FOR SEQ ID NO: 464:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:464:

TTATACTAGG TATGGTAAAT

20

(2) INFORMATION FOR SEQ ID NO: 465:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:465:

TATACTAGGT ATGGTAAATG

20

(2) INFORMATION FOR SEQ ID NO: 466:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:466:

ATACTAGGTA TGGTAAATGC

20

(2) INFORMATION FOR SEQ ID NO: 467:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:467:

TACTAGGTAT GGTAATGCA

20

(2) INFORMATION FOR SEQ ID NO: 468:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:468:

ACTAGGTATG GTAATGCAG

20

(2) INFORMATION FOR SEQ ID NO: 469:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:469:

CTAGGTATGG TAAATGCAGT

20

(2) INFORMATION FOR SEQ ID NO: 470:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:470:

TAGGTATGGT AAATGCAGTA

20

(2) INFORMATION FOR SEQ ID NO: 471:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:471:

AGGTATGGTA AATGCAGTAT

20

(2) INFORMATION FOR SEQ ID NO: 472:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:472:

GGTATGGTAA ATGCAGTATA

20

(2) INFORMATION FOR SEQ ID NO: 473:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:473:

GTATGGTAAA TGCACTATAC

20

(2) INFORMATION FOR SEQ ID NO: 474:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:474:

TATGGTAAAT GCAGTATACT

20

(2) INFORMATION FOR SEQ ID NO: 475:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:475:

ATGGTAAATG CAGTATACTT

20

(2) INFORMATION FOR SEQ ID NO: 476:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:476:

TGGTAAATGC AGTATACTTC

20

(2) INFORMATION FOR SEQ ID NO: 477:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:477:

GGTAAATGCA GTATACTTCC

20

(2) INFORMATION FOR SEQ ID NO: 478:

09784674.021501

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:478:

GTAAATGCAG TATACTTCCT

20

(2) INFORMATION FOR SEQ ID NO: 479:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:479:

TAAATGCAGT ATACTTCCTG

20

(2) INFORMATION FOR SEQ ID NO: 480:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:480:

AAATGCAGTA TACTTCCTGA

20

(2) INFORMATION FOR SEQ ID NO: 481:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:481:

AATGCAGTAT ACTTCCTGAA

20

(2) INFORMATION FOR SEQ ID NO: 482:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:482:

ATGCAGTATA CTTCCTGAAG

20

(2) INFORMATION FOR SEQ ID NO: 483:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

09784674-021501

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:483:

TGCAGTATAC TTCCTGAAGT

20

(2) INFORMATION FOR SEQ ID NO: 484:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:484:

GCAGTATACT TCCTGAAGTC

20

(2) INFORMATION FOR SEQ ID NO: 485:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:485:

CAGTATACTT CCTGAAGTCT

20

(2) INFORMATION FOR SEQ ID NO: 486:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:486:

AGTATACTTC CTGAAGTCTT

20

(2) INFORMATION FOR SEQ ID NO: 487:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:487:

GTATACTTCC TGAAGTCTTC

20

(2) INFORMATION FOR SEQ ID NO: 488:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:488:

TATACTTCCT GAAGTCTTCA

20

(2) INFORMATION FOR SEQ ID NO: 489:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:489:

ATACTTCCTG AAGTCTTCAT

20

(2) INFORMATION FOR SEQ ID NO: 490:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:490:

TACTTCTGA AGTCTTCATC

20

(2) INFORMATION FOR SEQ ID NO: 491:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:491:

ACTTCTGAA GTCTTCATCT

20

(2) INFORMATION FOR SEQ ID NO: 492:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:492:

CTTCCTGAAG TCTTCATCTA

20

(2) INFORMATION FOR SEQ ID NO: 493:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:493:

TTCCTGAAGT CTTTCATCTAA

20

(2) INFORMATION FOR SEQ ID NO: 494:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:494:

TCCTGAAGTC TTCATCTAAG

20

(2) INFORMATION FOR SEQ ID NO: 495:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs

0974674.021501

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:495:

CCTGAAGTCT TCATCTAAGG

20

(2) INFORMATION FOR SEQ ID NO: 496:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:496:

CTGAAGTCTT CATCTAAGGG

20

(2) INFORMATION FOR SEQ ID NO: 497:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:497:

TGAAGTCTTC ATCTAAGGGA

20

(2) INFORMATION FOR SEQ ID NO: 498:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:498:

GAAGTCTTCA TCTAAGGGAA

20

(2) INFORMATION FOR SEQ ID NO: 499:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:499:

AAGTCTTCAT CTAAGGGAAC

20

(2) INFORMATION FOR SEQ ID NO: 500:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:500:

09784674-021501

AGTCTTCATC TAAGGGAAC

20

(2) INFORMATION FOR SEQ ID NO: 501:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:501:

GTCTTCATCT AAGGGAAC

20

(2) INFORMATION FOR SEQ ID NO: 502:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:502:

TCTTCATCTA AGGGAAC

20

(2) INFORMATION FOR SEQ ID NO: 503:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:503:

CTTCATCTAA GGGAAGTGA

20

(2) INFORMATION FOR SEQ ID NO: 504:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:504:

TTTCATCTAAG GGGAAGTGA

20

(2) INFORMATION FOR SEQ ID NO: 505:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:505:

TCATCTAAGG GAAGTGA

20

(2) INFORMATION FOR SEQ ID NO: 506:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:506:

CATCTAAGGG AACTGAAAAA

20

(2) INFORMATION FOR SEQ ID NO: 507:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:507:

ATCTAAGGGA ACTGAAAAAT

20

(2) INFORMATION FOR SEQ ID NO: 508:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:508:

TCTAAGGGAA CTGAAAAATA

20

(2) INFORMATION FOR SEQ ID NO: 509:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:509:

CTAAGGGAAC TGA AAAATAT

20

(2) INFORMATION FOR SEQ ID NO: 510:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:510:

TAAGGGAAC TGA AAAATATG

20

(2) INFORMATION FOR SEQ ID NO: 511:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:511:

AAGGGAAC TGA AAAATATGC

20

(2) INFORMATION FOR SEQ ID NO: 512:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:512:

AGGGAACTGA AAAATATGCA

20

(2) INFORMATION FOR SEQ ID NO: 513:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:513:

GGGAACTGAA AAATATGCAT

20

(2) INFORMATION FOR SEQ ID NO: 514:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:514:

GGAAGTGAAG AAATATGCATC

20

(2) INFORMATION FOR SEQ ID NO: 515:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs

09764674-021501

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA  
(iii) HYPOTHETICAL: NO  
(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:515:

GAACTGAAAA ATATGCATCA

20

(2) INFORMATION FOR SEQ ID NO: 516:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
  
(ii) MOLECULE TYPE: cDNA  
(iii) HYPOTHETICAL: NO  
(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:516:

AACTGAAAAA TATGCATCAC

20

(2) INFORMATION FOR SEQ ID NO: 517:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
  
(ii) MOLECULE TYPE: cDNA  
(iii) HYPOTHETICAL: NO  
(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:517:

ACTGAAAAAT ATGCATCACC

20

(2) INFORMATION FOR SEQ ID NO: 518:

09784674-021501

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:518:

CTGAAAAATA TGCATCACCC

20

(2) INFORMATION FOR SEQ ID NO: 519:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:519:

TGAAAAATAT GCATCACCCA

20

(2) INFORMATION FOR SEQ ID NO: 520:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:520:

GAAAAATATG CATCACCCAC

20

(2) INFORMATION FOR SEQ ID NO: 521:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:521:

AAAAATATGC ATCACCCACA

20

(2) INFORMATION FOR SEQ ID NO: 522:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:522:

AAAATATGCA TCACCCACAT

20

(2) INFORMATION FOR SEQ ID NO: 523:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:523:

AAATATGCAT CACCCACATC

20

(2) INFORMATION FOR SEQ ID NO: 524:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:524:

AATATGCATC ACCCACATCC

20

(2) INFORMATION FOR SEQ ID NO: 525:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:525:

ATATGCATCA CCCACATCCA

20

(2) INFORMATION FOR SEQ ID NO: 526:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:526:

TATGCATCAC CCACATCCAG

20

(2) INFORMATION FOR SEQ ID NO: 527:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:527:

ATGCATCACC CACATCCAGT

20

(2) INFORMATION FOR SEQ ID NO: 528:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:528:

TGCATCACCC ACATCCAGTA

20

(2) INFORMATION FOR SEQ ID NO: 529:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:529:

GCATACCCA CATCCAGTAC

20

(2) INFORMATION FOR SEQ ID NO: 530:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:530:

CATCACCCAC ATCCAGTACT

20

(2) INFORMATION FOR SEQ ID NO: 531:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:531:

ATCACCCACA TCCAGTACTG

20

(2) INFORMATION FOR SEQ ID NO: 532:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

10971464-1-001501

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:532:

TCACCCACAT CCACTACTGT

20

(2) INFORMATION FOR SEQ ID NO: 533:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:533:

CACCCACATC CAGTACTGTT

20

(2) INFORMATION FOR SEQ ID NO: 534:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:534:

ACCCACATCC AGTACTGTTA

20

(2) INFORMATION FOR SEQ ID NO: 535:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs

03784674.021501

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:535:

CCCACATCCA GTACTGTTAC

20

(2) INFORMATION FOR SEQ ID NO: 536:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:536:

CCACATCCAG TACTGTTACT

20

(2) INFORMATION FOR SEQ ID NO: 537:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:537:

CACATCCAGT ACTGTTACTG

20

(2) INFORMATION FOR SEQ ID NO: 538:

10971464-1 021501

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:538:

ACATCCAGTA CTGTTACTGA

20

(2) INFORMATION FOR SEQ ID NO: 539:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:539:

CATCCAGTAC TGTTACTGAT

20

(2) INFORMATION FOR SEQ ID NO: 540:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:540:

09784674.021501

ATCCAGTACT GTTACTGATT

20

(2) INFORMATION FOR SEQ ID NO: 541:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:541:

TCCAGTACTG TTACTGATTT

20

(2) INFORMATION FOR SEQ ID NO: 542:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:542:

CCAGTACTGT TACTGATTTT

20

(2) INFORMATION FOR SEQ ID NO: 543:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

09784674.021504

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:543:

CAGTACTGTT ACTGATTTTT

20

(2) INFORMATION FOR SEQ ID NO: 544:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:544:

AGTACTGTGA CTGATTTTTT

20

(2) INFORMATION FOR SEQ ID NO: 545:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:545:

GTA CTGTAC TGATTTTTTC

20

(2) INFORMATION FOR SEQ ID NO: 546:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:546:

TACTGTTACT GATTTTTTCT

20

(2) INFORMATION FOR SEQ ID NO: 547:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:547:

ACTGTTACTG ATTTTTTCTT

20

(2) INFORMATION FOR SEQ ID NO: 548:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:548:

CTGTTACTGA TTTTTCCTTT

20

(2) INFORMATION FOR SEQ ID NO: 549:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

105720.14948260

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:549:

TGTTACTGAT TTTTCTTTT

20

(2) INFORMATION FOR SEQ ID NO: 550:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:550:

GTTACTGATT TTTTCTTTT

20

(2) INFORMATION FOR SEQ ID NO: 551:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:551:

TTACTGATTT TTTCTTTT

20

(2) INFORMATION FOR SEQ ID NO: 552:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:552:

TACTGATTTT TTCTTTTSTA

20

(2) INFORMATION FOR SEQ ID NO: 553:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:553:

ACTGATTTTT TCCTTTTSTA

20

(2) INFORMATION FOR SEQ ID NO: 554:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:554:

CTGATTTTTT CTTTTTAAAC

20

(2) INFORMATION FOR SEQ ID NO: 555:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:555:

TGATTTTTC TTTTAAACC

20

(2) INFORMATION FOR SEQ ID NO: 556:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:556:

GATTTTCT TTTTAAACC

20

(2) INFORMATION FOR SEQ ID NO: 557:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:557:

ATTTTCTT TTTTAAACCCT

20

(2) INFORMATION FOR SEQ ID NO: 558:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:558:

TTTTTCTTT TTAACCCCTG

20

(2) INFORMATION FOR SEQ ID NO: 559:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:559:

TTTTTCTTT TTAACCCCTGC

20

(2) INFORMATION FOR SEQ ID NO: 560:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:560:

TTTTCTTTTT TAACCTGCGG

20

(2) INFORMATION FOR SEQ ID NO: 561:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:561:

TTTCTTTTTT AACCTGCGG

20

(2) INFORMATION FOR SEQ ID NO: 562:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:562:

TTCTTTTTTA ACCCTGCGGG

20

(2) INFORMATION FOR SEQ ID NO: 563:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:563:

TCTTTTTTAA CCTGCGGGA

20

(2) INFORMATION FOR SEQ ID NO: 564:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:564:

CTTTTTTAAC CCTGCGGGAT

20

(2) INFORMATION FOR SEQ ID NO: 565:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:565:

TTTTTTAACC CTGCGGGATG

20

(2) INFORMATION FOR SEQ ID NO: 566:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:566:

TTTTTAACCC TCGGGGATGT

20

(2) INFORMATION FOR SEQ ID NO: 567:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:567:

TTTTAACCC TCGGGGATGTG

20

(2) INFORMATION FOR SEQ ID NO: 568:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:568:

TTTAACCC TCGGGGATGTGG

20

(2) INFORMATION FOR SEQ ID NO: 569:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:569:

TTAACCCCTGC GGGATGTGGT

20

(2) INFORMATION FOR SEQ ID NO: 570:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:570:

TAACCCCTGCG GGATGTGGTA

20

(2) INFORMATION FOR SEQ ID NO: 571:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:571:

AACCCCTGCGG GATGTGGTAT

20

(2) INFORMATION FOR SEQ ID NO: 572:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:572:

ACCCTGCGGG ATGTGGTATT

20

(2) INFORMATION FOR SEQ ID NO: 573:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:573:

CCCTGCGGGA TGTGGTATTC

20

(2) INFORMATION FOR SEQ ID NO: 574:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:574:

CCTGCGGGAT GTGGTATTC

20

(2) INFORMATION FOR SEQ ID NO: 575:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:575:

CTGCGGGATG TGGTATTCCT

20

(2) INFORMATION FOR SEQ ID NO: 576:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:576:

TGCGGGATGT GGTATTCCTA

20

(2) INFORMATION FOR SEQ ID NO: 577:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:577:

GCGGGATGTG GTATTCCTAA

20

(2) INFORMATION FOR SEQ ID NO: 578:

10971464-1.021501

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:578:

CGGGATGTGG TATTCTAAT

20

(2) INFORMATION FOR SEQ ID NO: 579:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:579:

GGGATGTGGT ATTCCTAATT

20

(2) INFORMATION FOR SEQ ID NO: 580:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:580:

GGATGTGGTA TTCCTAATTG

20

(2) INFORMATION FOR SEQ ID NO: 581:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:581:

GATGTGGTAT TCCTAATTGA

20

(2) INFORMATION FOR SEQ ID NO: 582:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:582:

ATGTGGTATT CCTAATTGAA

20

(2) INFORMATION FOR SEQ ID NO: 583:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

105720.42948260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:583:

TGTGGTATTC CTAATTGAAC

20

(2) INFORMATION FOR SEQ ID NO: 584:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:584:

GTGGTATTCC TAATTGAACT

20

(2) INFORMATION FOR SEQ ID NO: 585:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:585:

TGGTATTCCT AATTGAACTT

20

(2) INFORMATION FOR SEQ ID NO: 586:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:586:

GGTATTCCTA ATTGAACTTC

20

(2) INFORMATION FOR SEQ ID NO: 587:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:587:

GTATTCCTAA TTGAACTTCC

20

(2) INFORMATION FOR SEQ ID NO: 588:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:588:

TATTCCTAAT TGAAGTCC

20

(2) INFORMATION FOR SEQ ID NO: 589:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:589:

ATTCTTAATT GAATTCCCA

20

(2) INFORMATION FOR SEQ ID NO: 590:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:590:

TTCCTAATTG AACTTCCAG

20

(2) INFORMATION FOR SEQ ID NO: 591:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:591:

TCCTAATTGA ACTTCCAGA

20

(2) INFORMATION FOR SEQ ID NO: 592:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:592:

CCTAATTGAA CTCCCGAGAA

20

(2) INFORMATION FOR SEQ ID NO: 593:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:593:

CTAATTGAAC TTCCCGAAG

20

(2) INFORMATION FOR SEQ ID NO: 594:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:594:

TAATTGAACT TCCCGAAGT

20

(2) INFORMATION FOR SEQ ID NO: 595:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:595:

AATTGAACTT CCCAGAAGTC

20

(2) INFORMATION FOR SEQ ID NO: 596:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:596:

ATTGAACTTC CCAGAAGTCT

20

(2) INFORMATION FOR SEQ ID NO: 597:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:597:

TTGAACTTCC CAGAAGTCTT

20

(2) INFORMATION FOR SEQ ID NO: 598:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:598:

TGAACTTCCC AGAAGTCTTG

20

(2) INFORMATION FOR SEQ ID NO: 599:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:599:

GAAGTCTTGA

20

(2) INFORMATION FOR SEQ ID NO: 600:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:600:

AACTTCCCAG AAGTCTTGAG

20

(2) INFORMATION FOR SEQ ID NO: 601:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:601:

ACTTCCCAGA AGTCTTGAGT

20

(2) INFORMATION FOR SEQ ID NO: 602:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:602:

CTTCCCAGAA GTCTTGAGTT

20

(2) INFORMATION FOR SEQ ID NO: 603:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

09784674-021501

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:603:

TTCCCAGAAG TCTTGAGTTC

20

(2) INFORMATION FOR SEQ ID NO: 604:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:604:

TCCCAGAAGT CTTGAGTTCT

20

(2) INFORMATION FOR SEQ ID NO: 605:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:605:

CCCAGAAGTC TTGAGTTCTC

20

(2) INFORMATION FOR SEQ ID NO: 606:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:606:

CCAGAAGTCT TGAGTTCTCT

20

(2) INFORMATION FOR SEQ ID NO: 607:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:607:

CAGAAGTCTT GAGTTCTCTT

20

(2) INFORMATION FOR SEQ ID NO: 608:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:608:

AGAAGTCTTG AGTTCTCTTA

20

(2) INFORMATION FOR SEQ ID NO: 609:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:609:

GAAGTCTTGA GTTCTCTTAT

20

(2) INFORMATION FOR SEQ ID NO: 610:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:610:

AAGTCTTGAG TTCTCTTATT

20

(2) INFORMATION FOR SEQ ID NO: 611:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:611:

AGTCTTGAGT TCTCTTATTA

20

(2) INFORMATION FOR SEQ ID NO: 612:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:612:

GTCTTGAGTT CTCTTATTAA

20

(2) INFORMATION FOR SEQ ID NO: 613:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:613:

TCTTGAGTTC TCTTATTAAG

20

(2) INFORMATION FOR SEQ ID NO: 614:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:614:

CTTGAGTTCT CTTATTAAGT

20

(2) INFORMATION FOR SEQ ID NO: 615:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs

09784674.031501

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA  
(iii) HYPOTHETICAL: NO  
(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:615:

TTGAGTTCTC TTATTAAGTT

20

(2) INFORMATION FOR SEQ ID NO: 616:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
  
(ii) MOLECULE TYPE: cDNA  
(iii) HYPOTHETICAL: NO  
(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:616:

TGAGTTCTCT TATTAAGTTC

20

(2) INFORMATION FOR SEQ ID NO: 617:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
  
(ii) MOLECULE TYPE: cDNA  
(iii) HYPOTHETICAL: NO  
(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:617:

GAGTTCTCTT ATTAAGTTCT

20

(2) INFORMATION FOR SEQ ID NO: 618:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:618:

AGTTCTCTTA TTAAGTTCTC

20

(2) INFORMATION FOR SEQ ID NO: 619:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:619:

GTTCCTCTAT TAAGTTCTCT

20

(2) INFORMATION FOR SEQ ID NO: 620:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:620:

TTCTCTTATT AAGTTCTCTG

20

(2) INFORMATION FOR SEQ ID NO: 621:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:621:

TCTCTTATTA AGTTCTCTGA

20

(2) INFORMATION FOR SEQ ID NO: 622:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:622:

CTCTTATTAA GTTCTCTGAA

20

(2) INFORMATION FOR SEQ ID NO: 623:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

05704674.021504

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:623:

TCTTATTAAG TTCTCTGAAA

20

(2) INFORMATION FOR SEQ ID NO: 624:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:624:

CTTATTAAGT TCCTGAAAT

20

(2) INFORMATION FOR SEQ ID NO: 625:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:625:

TTATTAAGTT CTCTGAAATC

20

(2) INFORMATION FOR SEQ ID NO: 626:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:626:

TATTAAGTTC TCTGAAATCT

20

(2) INFORMATION FOR SEQ ID NO: 627:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:627:

ATTAAGTTCT CTGAAATCTA

20

(2) INFORMATION FOR SEQ ID NO: 628:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:628:

TTAAGTTCTC TGAAATCTAC

20

(2) INFORMATION FOR SEQ ID NO: 629:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:629:

TAAGTTCTCT GAAATCTACT

20

(2) INFORMATION FOR SEQ ID NO: 630:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:630:

AAGTTCTCTG AAATCTACTA

20

(2) INFORMATION FOR SEQ ID NO: 631:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:631:

AGTTCTCTGA AATCTACTAA

20

(2) INFORMATION FOR SEQ ID NO: 632:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:632:

GTTCTCTGAA ATCTACTAAT

20

(2) INFORMATION FOR SEQ ID NO: 633:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:633:

TTCTCTGAAA TCTACTAATT

20

(2) INFORMATION FOR SEQ ID NO: 634:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:634:

TCTCTGAAAT CTACTAATTT

20

(2) INFORMATION FOR SEQ ID NO: 635:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA  
(iii) HYPOTHETICAL: NO  
(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:635:

CTCTGAAATC TACTAATTTT

20

(2) INFORMATION FOR SEQ ID NO: 636:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
  
(ii) MOLECULE TYPE: cDNA  
(iii) HYPOTHETICAL: NO  
(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:636:

TCTGAAATCT ACTAATTTTC

20

(2) INFORMATION FOR SEQ ID NO: 637:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
  
(ii) MOLECULE TYPE: cDNA  
(iii) HYPOTHETICAL: NO  
(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:637:

CTGAAATCTA CTAATTTTCT

20

(2) INFORMATION FOR SEQ ID NO: 638:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:638:

TGAAATCTAC TAATTTCTC

20

(2) INFORMATION FOR SEQ ID NO: 639:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:639:

GAAATCTACT AATTTCTCC

20

(2) INFORMATION FOR SEQ ID NO: 640:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:640:

AAATCTACTA ATTTCTCCA

20

(2) INFORMATION FOR SEQ ID NO: 641:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:641:

AATCTACTAA TTTCTCCAT

20

(2) INFORMATION FOR SEQ ID NO: 642:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:642:

ATCTACTAAT TTTCTCCATT

20

(2) INFORMATION FOR SEQ ID NO: 643:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:643:

TCTACTAATT TTCTCCATT

20

(2) INFORMATION FOR SEQ ID NO: 644:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:644:

CTACTAATTT TCTCCATTTA

20

(2) INFORMATION FOR SEQ ID NO: 645:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:645:

TACTAATTTT CTCCATTAG

20

(2) INFORMATION FOR SEQ ID NO: 646:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:646:

ACTAATTTTC TCCATTAGT

20

(2) INFORMATION FOR SEQ ID NO: 647:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:647:

CTAATTTTCT CCATTAGTGA

20

(2) INFORMATION FOR SEQ ID NO: 648:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:648:

TAATTTTCTC CATTTAGTAC

20

(2) INFORMATION FOR SEQ ID NO: 649:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:649:

AATTTTCTCC ATTTAGTACT

20

(2) INFORMATION FOR SEQ ID NO: 650:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:650:

ATTTTCTCCA TTTAGTACTG

20

(2) INFORMATION FOR SEQ ID NO: 651:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:651:

TTTTCTCCAT TTAGTACTGT

20

(2) INFORMATION FOR SEQ ID NO: 652:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:652:

TTTCTCCATT TAGTACTGTC

20

(2) INFORMATION FOR SEQ ID NO: 653:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:653:

TTCTCCATTT AGTACTGTCT

20

(2) INFORMATION FOR SEQ ID NO: 654:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:654:

TCTCCATTTA GTACTGTCTT

20

(2) INFORMATION FOR SEQ ID NO: 655:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs

105120-14948420

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:655:

CTCCATTAG TACTGTCTTT

20

(2) INFORMATION FOR SEQ ID NO: 656:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:656:

TCCATTAGT ACTGTCTTTT

20

(2) INFORMATION FOR SEQ ID NO: 657:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:657:

CCATTAGTA CTGTCTTTTT

20

(2) INFORMATION FOR SEQ ID NO: 658:

097844574-021501

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:658:

CATTAGTAC TGTCTTTTT

20

(2) INFORMATION FOR SEQ ID NO: 659:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:659:

ATTAGTACT GTCITTTTT

20

(2) INFORMATION FOR SEQ ID NO: 660:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:660:

09781464-1021501

TTTAGTACTG TCTTTTCTT

20

(2) INFORMATION FOR SEQ ID NO: 661:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:661:

TTAGTACTGT CTTTCTCTT

20

(2) INFORMATION FOR SEQ ID NO: 662:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:662:

TAGTACTGTC TTTTCTCTT

20

(2) INFORMATION FOR SEQ ID NO: 663:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:663:

AGTACTGTCT TTTTCTTTA

20

(2) INFORMATION FOR SEQ ID NO: 664:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:664:

GTACTGTCTT TTTTCTTTAT

20

(2) INFORMATION FOR SEQ ID NO: 665:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:665:

TACTGTCTTT TTTCTTTATG

20

(2) INFORMATION FOR SEQ ID NO: 666:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:666:

ACTGTCTTTT TTCTTTATGG

20

(2) INFORMATION FOR SEQ ID NO: 667:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:667:

CTGTCTTTT TCTTTATGGC

20

(2) INFORMATION FOR SEQ ID NO: 668:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:668:

TGTCTTTTTT CTTTATGGCA

20

(2) INFORMATION FOR SEQ ID NO: 669:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:669:

GTCTTTTTTC TTTATGGCAA

20

(2) INFORMATION FOR SEQ ID NO: 670:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:670:

TCTTTTTTCT TTATGGCAAA

20

(2) INFORMATION FOR SEQ ID NO: 671:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:671:

CTTTTTTCTT TATGGCAAAAT

20

(2) INFORMATION FOR SEQ ID NO: 672:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:672:

TTTTTCTTT ATGGCAAATA

20

(2) INFORMATION FOR SEQ ID NO: 673:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:673:

TTTTTCTTTA TGGCAAATAC

20

(2) INFORMATION FOR SEQ ID NO: 674:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:674:

TTTTCTTAT GGCAAATACT

20

(2) INFORMATION FOR SEQ ID NO: 675:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:675:

TTTCTTTATG GCAAATACTG

20

(2) INFORMATION FOR SEQ ID NO: 676:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:676:

TTCTTTATGG CAAATACTGG

20

(2) INFORMATION FOR SEQ ID NO: 677:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:677:

TCCTTTATGGC AAATACTGGA

20

(2) INFORMATION FOR SEQ ID NO: 678:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:678:

CTTTATGGCA AATACTGGAG

20

(2) INFORMATION FOR SEQ ID NO: 679:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:679:

TTTATGGCAA ATACTGGAGT

20

(2) INFORMATION FOR SEQ ID NO: 680:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:680:

09704674.021501

TTATGGCAAA TACTGGAGTA

20

(2) INFORMATION FOR SEQ ID NO: 681:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:681:

TATGGCAAAT ACTGGAGTAT

20

(2) INFORMATION FOR SEQ ID NO: 682:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:682:

ATGGCAAATA CTGGAGTATT

20

(2) INFORMATION FOR SEQ ID NO: 683:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:683:

TGGCAAATAC TGGAGTATTG

20

(2) INFORMATION FOR SEQ ID NO: 684:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:684:

GGCAAATACT GGAGTATTGT

20

(2) INFORMATION FOR SEQ ID NO: 685:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:685:

GCAAATACTG GAGTATTGTA

20

(2) INFORMATION FOR SEQ ID NO: 686:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:686:

CAAATACTGG AGTATTGTAT

20

(2) INFORMATION FOR SEQ ID NO: 687:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:687:

AAATACTGGA GTATTGTATG

20

(2) INFORMATION FOR SEQ ID NO: 688:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:688:

AATACTGGAG TATTGTAITG

20

(2) INFORMATION FOR SEQ ID NO: 689:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:689:

ATACTGGAGT ATTGTATGGA

20

(2) INFORMATION FOR SEQ ID NO: 690:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:690:

TACTGGAGTA TTGTATGGAT

20

(2) INFORMATION FOR SEQ ID NO: 691:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:691:

ACTGGAGTAT TGTATGGATT

20

(2) INFORMATION FOR SEQ ID NO: 692:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:692:

CTGGAGTATT GTATGGATTCT

20

(2) INFORMATION FOR SEQ ID NO: 693:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:693:

TGGAGTATTG TATGGATTCT

20

(2) INFORMATION FOR SEQ ID NO: 694:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:694:

GGAGTATTGT ATGGATTCTC

20

(2) INFORMATION FOR SEQ ID NO: 695:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:695:

GAGTATTGTA TGGATTCTCA

20

(2) INFORMATION FOR SEQ ID NO: 696:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:696:

AGTATTGTAT GGATTCTCAG

20

(2) INFORMATION FOR SEQ ID NO: 697:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:697:

GIATTGTATG GATTCTCAGG

20

(2) INFORMATION FOR SEQ ID NO: 698:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
  
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:698:

TATTGTATGG ATTCTCAGGC

20

(2) INFORMATION FOR SEQ ID NO: 699:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
  
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:699:

ATTGTATGGA TTCTCAGGCC

20

(2) INFORMATION FOR SEQ ID NO: 700:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
  
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:700:

TTGTATGGAT TCTCAGGCCC

20

(2) INFORMATION FOR SEQ ID NO: 701:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:701:

TGTATGGATT CTCAGGCCCA

20

(2) INFORMATION FOR SEQ ID NO: 702:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:702:

GTATGGATTCTCAGGCCCAA

20

(2) INFORMATION FOR SEQ ID NO: 703:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:703:

TATGGATTCT CAGGCCCAAT

20

(2) INFORMATION FOR SEQ ID NO: 704:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:704:

ATGGATTCTC AGGCCCAATT

20

(2) INFORMATION FOR SEQ ID NO: 705:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:705:

TGGATTCTCA GGCCCAATTT

20

(2) INFORMATION FOR SEQ ID NO: 706:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:706:

GGATTCTCAG GCCCAATTTT

20

(2) INFORMATION FOR SEQ ID NO: 707:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:707:

GATTCTCAGG CCCAATTTT

20

(2) INFORMATION FOR SEQ ID NO: 708:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:708:

ATTCTCAGGC CCAATTTTG

20

(2) INFORMATION FOR SEQ ID NO: 709:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:709:

TTCTCAGGCC CAATTTTGA

20

(2) INFORMATION FOR SEQ ID NO: 710:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:710:

TCTCAGGCC AATTTTGA

20

(2) INFORMATION FOR SEQ ID NO: 711:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:711:

CTCAGGCCA ATTTTGA

20

(2) INFORMATION FOR SEQ ID NO: 712:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:712:

TCAGGCCCAA TTTTGAAAT

20

(2) INFORMATION FOR SEQ ID NO: 713:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:713:

CAGGCCCAAT TTTTGAAAT

20

(2) INFORMATION FOR SEQ ID NO: 714:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:714:

AGGCCCAATT TTTGAAATTT

20

(2) INFORMATION FOR SEQ ID NO: 715:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:715:

GGCCCAATTT TTGAAATTTT

20

(2) INFORMATION FOR SEQ ID NO: 716:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:716:

GCCCAATTTT TGAAATTTTC

20

(2) INFORMATION FOR SEQ ID NO: 717:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:717:

CCCAATTTT GAAATTTTCC

20

(2) INFORMATION FOR SEQ ID NO: 718:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:718:

CCAATTTTGG AAATTTCC

20

(2) INFORMATION FOR SEQ ID NO: 719:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:719:

CAATTTTGA AATTTCCCT

20

(2) INFORMATION FOR SEQ ID NO: 720:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:720:

AATTTTGGAA ATTTCCCTT

20

(2) INFORMATION FOR SEQ ID NO: 721:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:721:

ATTTTGGAAA TTTCCCTTC

20

(2) INFORMATION FOR SEQ ID NO: 722:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:722:

TTTTTGAAT TTTCCCTTC

20

(2) INFORMATION FOR SEQ ID NO: 723:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:723:

TTTGAAATT TTCCCTTCCT

20

(2) INFORMATION FOR SEQ ID NO: 724:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:724:

TTTGAAATTT TCCCTTCCTT

20

(2) INFORMATION FOR SEQ ID NO: 725:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:725:

TTGAAATTTT CCCTTCCTTT

20

(2) INFORMATION FOR SEQ ID NO: 726:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:726:

TGAAATTTTC CCTTCTTTT

20

(2) INFORMATION FOR SEQ ID NO: 727:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:727:

GAAATTTTCC CTCCTTTTC

20

(2) INFORMATION FOR SEQ ID NO: 728:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:728:

AAATTTTCCC TTCCTTTTCC

20

(2) INFORMATION FOR SEQ ID NO: 729:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:729:

AATTTCCCT TCCTTTCCA

20

(2) INFORMATION FOR SEQ ID NO: 730:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:730:

ATTTCCCTT CCTTTCCAT

20

(2) INFORMATION FOR SEQ ID NO: 731:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:731:

TTTCCCTTC CTTTCCATT

20

(2) INFORMATION FOR SEQ ID NO: 732:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

09784674-021501  
105120.4244260

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:732:

TTTCCCTTCC TTTTCATT

20

(2) INFORMATION FOR SEQ ID NO: 733:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:733:

TTCCCTTCCT TTTCCATTTC

20

(2) INFORMATION FOR SEQ ID NO: 734:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:734:

TCCCTTCCTT TTCCATTTC

20

(2) INFORMATION FOR SEQ ID NO: 735:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs

10971464-1

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:735:

CCCTTCCTTT TCATTCTG

20

(2) INFORMATION FOR SEQ ID NO: 736:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:736:

CCTTCCTTTT CCATTCTGT

20

(2) INFORMATION FOR SEQ ID NO: 737:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:737:

CTTCCTTTTC CATTCTGTGTA

20

(2) INFORMATION FOR SEQ ID NO: 738:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:738:

TTCCTTTTCC ATTTCTGTAC

20

(2) INFORMATION FOR SEQ ID NO: 739:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:739:

TCCTTTTCCA TTCTGTACA

20

(2) INFORMATION FOR SEQ ID NO: 740:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:740:

10971464-1-021501

CCTTTTCCAT TTCTGTACAA

20

(2) INFORMATION FOR SEQ ID NO: 741:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:741:

CTTTTCCATT TCTGTACAA

20

(2) INFORMATION FOR SEQ ID NO: 742:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:742:

TTTTCCATT CTGTACAAAT

20

(2) INFORMATION FOR SEQ ID NO: 743:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:743:

TTCCATTTC TGACAAATT

20

(2) INFORMATION FOR SEQ ID NO: 744:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:744:

TTCCATTCT GTACAAATT

20

(2) INFORMATION FOR SEQ ID NO: 745:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:745:

TCCATTCTG TACAAATT

20

(2) INFORMATION FOR SEQ ID NO: 746:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:746:

CCATTCTGT ACAAAATTTCT

20

(2) INFORMATION FOR SEQ ID NO: 747:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:747:

CATTCTGTA CAAATTTCTA

20

(2) INFORMATION FOR SEQ ID NO: 748:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:748:

ATTCTGTAC AAATTTCTAC

20

(2) INFORMATION FOR SEQ ID NO: 749:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

105120-1464262

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:749:

TTTCTGTACA AATTCTACT

20

(2) INFORMATION FOR SEQ ID NO: 750:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:750:

TTTCTGTACAA ATTCTACTA

20

(2) INFORMATION FOR SEQ ID NO: 751:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:751:

TCTGTACAAA TTTCTACTAA

20

(2) INFORMATION FOR SEQ ID NO: 752:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:752:

CTGTACAAAT TTCTACTAAT

20

(2) INFORMATION FOR SEQ ID NO: 753:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:753:

TGTACAAATT TCTACTAATG

20

(2) INFORMATION FOR SEQ ID NO: 754:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:754:

GTACAAATTT CTACTAATGC

20

(2) INFORMATION FOR SEQ ID NO: 755:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:755:

TACAAATTTC TACTAATGCT

20

(2) INFORMATION FOR SEQ ID NO: 756:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:756:

ACAAATTCTCT ACTAATGCTT

20

(2) INFORMATION FOR SEQ ID NO: 757:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:757:

CAAATTCTCTA CTAATGCTTT

20

(2) INFORMATION FOR SEQ ID NO: 758:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
  
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:758:

AAATTCTAC TAATGCTTTT

20

(2) INFORMATION FOR SEQ ID NO: 759:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:759:

AATTCTACT AATGCTTTTA

20

(2) INFORMATION FOR SEQ ID NO: 760:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:760:

09784674.021501

ATTCTACTA ATGCTTTTAT

20

(2) INFORMATION FOR SEQ ID NO: 761:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:761:

TTTCTACTAA TGCTTTTATT

20

(2) INFORMATION FOR SEQ ID NO: 762:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:762:

TTCTACTAAT GCTTTTATT

20

(2) INFORMATION FOR SEQ ID NO: 763:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

09784674.021501

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:763:

TCTACTAATG CTTTATATTT

20

(2) INFORMATION FOR SEQ ID NO: 764:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:764:

CTACTAATGC TTTTATTTTT

20

(2) INFORMATION FOR SEQ ID NO: 765:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:765:

TACTAATGCT TTTATTTTTT

20

(2) INFORMATION FOR SEQ ID NO: 766:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:766:

ACTAATGCCTT TTATTTTTC

20

(2) INFORMATION FOR SEQ ID NO: 767:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:767:

CTAATGCTTT TATTTTTC

20

(2) INFORMATION FOR SEQ ID NO: 768:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:768:

TAATGCTTTT ATTTTTC

20

(2) INFORMATION FOR SEQ ID NO: 769:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:769:

AATGCTTTTA TTTTCTTC

20

(2) INFORMATION FOR SEQ ID NO: 770:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:770:

ATGCTTTTAT TTTTCTTCT

20

(2) INFORMATION FOR SEQ ID NO: 771:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:771:

TGCTTTTATT TTTTCTTCTG

20

(2) INFORMATION FOR SEQ ID NO: 772:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:772:

GCITTTATTT TTTCTTCTGT

20

(2) INFORMATION FOR SEQ ID NO: 773:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:773:

CTTTTATTTT TTCTTCTGTC

20

(2) INFORMATION FOR SEQ ID NO: 774:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:774:

TTTTTATTTT TCTTCTGTCA

20

(2) INFORMATION FOR SEQ ID NO: 775:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs

10971464-1

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:775:

TTTATTTTTT CTCTGTCAA

20

(2) INFORMATION FOR SEQ ID NO: 776:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:776:

TTATTTTTTC TTCTGTCAAT

20

(2) INFORMATION FOR SEQ ID NO: 777:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:777:

TATTTTTTCT TCTGTCAATG

20

(2) INFORMATION FOR SEQ ID NO: 778:

09784674.021501

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
  
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:778:

ATTTTTCTT CTGCAATGG

20

(2) INFORMATION FOR SEQ ID NO: 779:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
  
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:779:

TTTTTCTTC TGCAATGGC

20

(2) INFORMATION FOR SEQ ID NO: 780:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
  
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:780:

TTTTTCTTCT GTCAATGGCC

20

(2) INFORMATION FOR SEQ ID NO: 781:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:781:

TTTCTTCTG TCAATGGCCA

20

(2) INFORMATION FOR SEQ ID NO: 782:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:782:

TTTCTTCTGT CAATGGCCAT

20

(2) INFORMATION FOR SEQ ID NO: 783:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:783:

TTCTTCTGTC AATGGCCATT

20

(2) INFORMATION FOR SEQ ID NO: 784:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:784:

TCTTCTGTCA ATGGCCATTG

20

(2) INFORMATION FOR SEQ ID NO: 785:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:785:

CTTCTGTCAA TGGCCATTGT

20

(2) INFORMATION FOR SEQ ID NO: 786:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:786:

TTCTGTCAAT GCCATTGTT

20

(2) INFORMATION FOR SEQ ID NO: 787:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:787:

TCTGTCAATG GCCATTGTTT

20

(2) INFORMATION FOR SEQ ID NO: 788:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:788:

CTGTCAATGG CCATTGTTTA

20

(2) INFORMATION FOR SEQ ID NO: 789:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:789:

TGTCAATGGC CATTGTTTAA

20

(2) INFORMATION FOR SEQ ID NO: 790:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:790:

GTCAATGGCC ATTGTTTAAAC

20

(2) INFORMATION FOR SEQ ID NO: 791:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:791:

TCAATGGCCA TTGTTTAACT

20

(2) INFORMATION FOR SEQ ID NO: 792:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:792:

CAATGGCCAT TGTTAACTT

20

(2) INFORMATION FOR SEQ ID NO: 793:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:793:

AATGGCCATT GTTTAACTTT

20

(2) INFORMATION FOR SEQ ID NO: 794:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:794:

ATGGCCATTG TTTAACTTTT

20

(2) INFORMATION FOR SEQ ID NO: 795:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:795:

TGGCCATTGT TTAACCTTTG

20

(2) INFORMATION FOR SEQ ID NO: 796:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:796:

GGCCATTGTT TAACCTTTGG

20

(2) INFORMATION FOR SEQ ID NO: 797:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:797:

GCCATTGTTT AACCTTTGGG

20

(2) INFORMATION FOR SEQ ID NO: 798:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:798:

CCATTGTTTA ACTTTGGGC

20

(2) INFORMATION FOR SEQ ID NO: 799:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:799:

CATTGTTTAA CTTTGGGCC

20

(2) INFORMATION FOR SEQ ID NO: 800:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:800:

ATTGTTTAAC TTTGGGCCA

20

(2) INFORMATION FOR SEQ ID NO: 801:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:801:

TTGTTTAACT TTTGGGCCAT

20

(2) INFORMATION FOR SEQ ID NO: 802:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:802:

TGTTTAACTT TTGGGCCATC

20

(2) INFORMATION FOR SEQ ID NO: 803:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:803:

GTTTAACTTT TGGGCCATCC

20

(2) INFORMATION FOR SEQ ID NO: 804:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:804:

TTTAACTTTT GGGCCATCCA

20

(2) INFORMATION FOR SEQ ID NO: 805:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:805:

TTAACTTTTG GGCCATCCAT

20

(2) INFORMATION FOR SEQ ID NO: 806:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:806:

TAACTTTTGG GCCATCCATT

20

(2) INFORMATION FOR SEQ ID NO: 807:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:807:

AACTTTTGGG CCATCCATTC

20

(2) INFORMATION FOR SEQ ID NO: 808:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:808:

ACTTTTGGGC CATCCATTCC

20

(2) INFORMATION FOR SEQ ID NO: 809:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:809:

CTTTTGGGCC ATCCATTCCT

20

(2) INFORMATION FOR SEQ ID NO: 810:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:810:

TTTGGGCCA TCCATTCCTG

20

(2) INFORMATION FOR SEQ ID NO: 811:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:811:

TTTGGGCCAT CCATTCCTGG

20

(2) INFORMATION FOR SEQ ID NO: 812:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:812:

TTGGGCCATC CATTCTGGC

20

(2) INFORMATION FOR SEQ ID NO: 813:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:813:

TGGGCCATCC ATTCTGGCT

20

(2) INFORMATION FOR SEQ ID NO: 814:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:814:

GGGCCATCCA TTCCTGGCTT

20

(2) INFORMATION FOR SEQ ID NO: 815:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs

10971464-021501

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:815:

GGCCATCCAT TCCTGGCTTT

20

(2) INFORMATION FOR SEQ ID NO: 816:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:816:

GCCATCCATT CCTGGCTTTA

20

(2) INFORMATION FOR SEQ ID NO: 817:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:817:

CCATCCATTC CTGGCTTTAA

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(2) INFORMATION FOR SEQ ID NO: 818:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:818:

CATCCATTCC TGGCTTTAAT

20

(2) INFORMATION FOR SEQ ID NO: 819:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:819:

ATCCATTCCT GGCTTTAATT

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(2) INFORMATION FOR SEQ ID NO: 820:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:820:

10971464-021501

TCCATTCCTG GCTTTAATTT

20

(2) INFORMATION FOR SEQ ID NO: 821:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:821:

CCATTCCTGG CTTTAATTTT

20

(2) INFORMATION FOR SEQ ID NO: 822:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:822:

CATTCCTGGC TTTAATTTTA

20

(2) INFORMATION FOR SEQ ID NO: 823:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

10971464-1 021501

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:823:

ATTCTTGGCT TTAATTTTAC

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(2) INFORMATION FOR SEQ ID NO: 824:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:824:

TTCTCTGGCTT TAATTTTACT

20

(2) INFORMATION FOR SEQ ID NO: 825:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:825:

TCCTTGGCTTT AATTTTACTG

20

(2) INFORMATION FOR SEQ ID NO: 826:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

09784674-02504  
10520 4798760

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:826:

CCTGGCTTTA ATTTTACTGG

20

(2) INFORMATION FOR SEQ ID NO: 827:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:827:

CTGGCTTTAA TTTTACTGGT

20

(2) INFORMATION FOR SEQ ID NO: 828:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:828:

TGGCTTTAAT TTTACTGGTA

20

(2) INFORMATION FOR SEQ ID NO: 829:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:829:

GGCTTTAATT TTACTGGTAC

20

(2) INFORMATION FOR SEQ ID NO: 830:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:830:

GCTTTAATTT TACTGGTACA

20

(2) INFORMATION FOR SEQ ID NO: 831:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:831:

CTTTAATTTT ACTGGTACAG

20

(2) INFORMATION FOR SEQ ID NO: 832:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:832:

TTTAATTTTA CTGGTACAGT

20

(2) INFORMATION FOR SEQ ID NO: 833:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:833:

TTAATTTTAC TGGTACAGTC

20

(2) INFORMATION FOR SEQ ID NO: 834:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:834:

TAATTTTACT GGTACAGTCT

20

(2) INFORMATION FOR SEQ ID NO: 835:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:835:

AATTTTACTG GTACAGTCTC

20

(2) INFORMATION FOR SEQ ID NO: 836:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:836:

ATTTTACTGG TACAGICTCA

20

(2) INFORMATION FOR SEQ ID NO: 837:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:837:

TTTTACTGGT ACAGTCTCAA

20

(2) INFORMATION FOR SEQ ID NO: 838:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:838:

TTTACTGGTA CAGTCTCAAT

20

(2) INFORMATION FOR SEQ ID NO: 839:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:839:

TTTACTGGTAC AGTCTCAATA

20

(2) INFORMATION FOR SEQ ID NO: 840:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:840:

TACTGGTACA GTCTCAATAG

20

(2) INFORMATION FOR SEQ ID NO: 841:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:841:

ACTGGTACAG TCTCAATAGG

20

(2) INFORMATION FOR SEQ ID NO: 842:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:842:

CTGGTACAGT CTCAATAGGG

20

(2) INFORMATION FOR SEQ ID NO: 843:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:843:

TGGTACAGTC TCAATAGGGC

20

(2) INFORMATION FOR SEQ ID NO: 844:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:844:

GGTACAGTCT CAATAGGGCT

20

(2) INFORMATION FOR SEQ ID NO: 845:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:845:

GTACAGTCTC AATAGGGCTA

20

(2) INFORMATION FOR SEQ ID NO: 846:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:846:

TACAGTCTCA ATAGGGCTAA

20

(2) INFORMATION FOR SEQ ID NO: 847:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:847:

ACAGTCTCAA TAGGGCTAAT

20

(2) INFORMATION FOR SEQ ID NO: 848:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:848:

CAGTCTCAAT AGGGCTAATG

20

(2) INFORMATION FOR SEQ ID NO: 849:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:849:

AGTCTCAATA GGGCTAATGG

20

(2) INFORMATION FOR SEQ ID NO: 850:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:850:

GTCTCAATAG GGCTAATGGG

20

(2) INFORMATION FOR SEQ ID NO: 851:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:851:

TCTCAATAGG GCTAATGGGA

20

(2) INFORMATION FOR SEQ ID NO: 852:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

09784674.021501

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:852:

CTCAATAGGG CTAATGGGAA

20

(2) INFORMATION FOR SEQ ID NO: 853:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:853:

TCAATAGGGC TAATGGGAAA

20

(2) INFORMATION FOR SEQ ID NO: 854:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:854:

CAATAGGGCT AATGGGAAAA

20

(2) INFORMATION FOR SEQ ID NO: 855:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:855:

AATAGGGCTA ATGGGAAAT

20

(2) INFORMATION FOR SEQ ID NO: 856:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:856:

ATAGGGCTAA TGGGAAAT

20

(2) INFORMATION FOR SEQ ID NO: 857:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:857:

TAGGGCTAAT GGGAAATTT

20

(2) INFORMATION FOR SEQ ID NO: 858:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:858:

AGGGCTAATG GGAAATTTA

20

(2) INFORMATION FOR SEQ ID NO: 859:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:859:

GGGCTAATGG GAAATTTAA

20

(2) INFORMATION FOR SEQ ID NO: 860:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:860:

09784674-023501

GGCTAATGGG AAAATTTAAA

20

(2) INFORMATION FOR SEQ ID NO: 861:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:861:

GCTAATGGGA AAATTTAAG

20

(2) INFORMATION FOR SEQ ID NO: 862:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:862:

CTAATGGGAA AATTTAAAGT

20

(2) INFORMATION FOR SEQ ID NO: 863:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:863:

TAATGGGAAA ATTTAAAGTG

20

(2) INFORMATION FOR SEQ ID NO: 864:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:864:

AATGGGAAAA TTAAAGTGC

20

(2) INFORMATION FOR SEQ ID NO: 865:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:865:

ATGGGAAAAT TTAAAGTGCA

20

(2) INFORMATION FOR SEQ ID NO: 866:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:866:

TGGGAAAATT TAAAGTGCAA

20

(2) INFORMATION FOR SEQ ID NO: 867:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:867:

GGGAAAATTT AAAGTGCAAC

20

(2) INFORMATION FOR SEQ ID NO: 868:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:868:

GGAAAATTTA AAGTGAACC

20

(2) INFORMATION FOR SEQ ID NO: 869:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:869:

GAAAAATTAA AGTGCAACCA

20

(2) INFORMATION FOR SEQ ID NO: 870:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:870:

AAAATTTAAA GTGCAACCA

20

(2) INFORMATION FOR SEQ ID NO: 871:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:871:

AAATTTAAAG TGCAACCAAT

20

(2) INFORMATION FOR SEQ ID NO: 872:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:872:

AATTTAAAGT GCAACCAATC

20

(2) INFORMATION FOR SEQ ID NO: 873:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:873:

ATTTAAAGTG CAACCAATCT

20

(2) INFORMATION FOR SEQ ID NO: 874:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:874:

TTTAAAGTGC AACCAATCTG

20

(2) INFORMATION FOR SEQ ID NO: 875:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs

09784674-021504

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:875:

TTAAAGTGCA ACCAATCTGA

20

(2) INFORMATION FOR SEQ ID NO: 876:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:876:

TAAAGTGCAA CCAATCTGAG

20

(2) INFORMATION FOR SEQ ID NO: 877:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:877:

AAAGTGCAAC CAATCTGAGT

20

(2) INFORMATION FOR SEQ ID NO: 878:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:878:

AAGTGCAACC AATCTGAGTC

20

(2) INFORMATION FOR SEQ ID NO: 879:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:879:

AGTGCAACCA ATCTGAGTCA

20

(2) INFORMATION FOR SEQ ID NO: 880:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:880:

105120-4248260

GTGCAACCAA TCTGAGTCAA

20

(2) INFORMATION FOR SEQ ID NO: 881:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:881:

TGCAACCAAT CTGAGTCAAC

20

(2) INFORMATION FOR SEQ ID NO: 882:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:882:

GCAACCAATC TGAGTCAACA

20

(2) INFORMATION FOR SEQ ID NO: 883:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:883:

CAACCAATCT GAGTCAACAG

20

(2) INFORMATION FOR SEQ ID NO: 884:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:884:

AACCAATCTG AGTCAACAGA

20

(2) INFORMATION FOR SEQ ID NO: 885:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:885:

ACCAATCTGA GTCAACAGAT

20

(2) INFORMATION FOR SEQ ID NO: 886:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:886:

CCAATCTGAG TCAACAGATT

20

(2) INFORMATION FOR SEQ ID NO: 887:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:887:

CAATCTGAGT CAACAGATT

20

(2) INFORMATION FOR SEQ ID NO: 888:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:888:

AATCTGAGTC AACAGATTTC

20

(2) INFORMATION FOR SEQ ID NO: 889:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:889:

ATCTGAGTCA ACAGATTCTC

20

(2) INFORMATION FOR SEQ ID NO: 890:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:890:

TCTGAGTCAA CAGATTCTT

20

(2) INFORMATION FOR SEQ ID NO: 891:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:891:

CTGAGTCAAC AGATTTCTTC

20

(2) INFORMATION FOR SEQ ID NO: 892:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:892:

TGAGTCAACA GATTCTTCC

20

(2) INFORMATION FOR SEQ ID NO: 893:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:893:

GAGTCAACAG ATTCTTCCA

20

(2) INFORMATION FOR SEQ ID NO: 894:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:894:

AGTCAACAGA TTTCTTCCAA

20

(2) INFORMATION FOR SEQ ID NO: 895:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:895:

GTCAACAGAT TTCTTCCAAT

20

(2) INFORMATION FOR SEQ ID NO: 896:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:896:

TCAACAGATT TCTTCCAATT

20

(2) INFORMATION FOR SEQ ID NO: 897:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:897:

CAACAGATTT CTTCGAATTA

20

(2) INFORMATION FOR SEQ ID NO: 898:

09784674-021501

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:898:

AACAGATTTT TTCCAATTAT

20

(2) INFORMATION FOR SEQ ID NO: 899:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:899:

ATCAGATTCT TCCAATTATG

20

(2) INFORMATION FOR SEQ ID NO: 900:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:900:

00784674.021501  
105120.1294620

CAGATTCTT CCAATTATGT

20

(2) INFORMATION FOR SEQ ID NO: 901:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:901:

AGATTCTTC CAATTATGTT

20

(2) INFORMATION FOR SEQ ID NO: 902:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:902:

GATTCTTCC AATTATGTTG

20

(2) INFORMATION FOR SEQ ID NO: 903:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:903:

ATTTCTTCCA ATTATGTTGA

20

(2) INFORMATION FOR SEQ ID NO: 904:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:904:

TTTCTTCCAA TTATGTTGAC

20

(2) INFORMATION FOR SEQ ID NO: 905:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:905:

TTCTTCCAAT TATGTTGACA

20

(2) INFORMATION FOR SEQ ID NO: 906:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:906:

TCTTCCAATT ATGTTGACAG

20

(2) INFORMATION FOR SEQ ID NO: 907:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:907:

CTTCCAATTA TGTGACAGG

20

(2) INFORMATION FOR SEQ ID NO: 908:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:908:

TTCCAATTAT GTTGACAGGT

20

(2) INFORMATION FOR SEQ ID NO: 909:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:909:

TCCAATTATG TTGACAGGTG

20

(2) INFORMATION FOR SEQ ID NO: 910:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:910:

CCAATTATGT TGACAGGTG

20

(2) INFORMATION FOR SEQ ID NO: 911:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:911:

CAATTATGTT GACAGGTGTA

20

(2) INFORMATION FOR SEQ ID NO: 912:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:912:

AATTATGTTG ACAGGTGTAG

20

(2) INFORMATION FOR SEQ ID NO: 913:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:913:

ATTATGTTGA CAGGTGTAGG

20

(2) INFORMATION FOR SEQ ID NO: 914:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:914:

TTATGTTGAC AGGTGTAGGT

20

(2) INFORMATION FOR SEQ ID NO: 915:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs

09784674.02500

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:915:

TATGTTGACA GGTGTAGGTC

20

(2) INFORMATION FOR SEQ ID NO: 916:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:916:

ATGTTGACAG GTGTAGGTCC

20

(2) INFORMATION FOR SEQ ID NO: 917:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:917:

TGTTGACAGG TGTAGGTCCT

20

(2) INFORMATION FOR SEQ ID NO: 918:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:918:

GTTGACAGGT GTAGGTCCTA

20

(2) INFORMATION FOR SEQ ID NO: 919:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:919:

TTGACAGGTG TAGGTCCTAC

20

(2) INFORMATION FOR SEQ ID NO: 920:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:920:

09784674.021501  
105720\*42948260

TGACAGGTGT AGGTCCTACT

20

(2) INFORMATION FOR SEQ ID NO: 921:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:921:

GACAGGTGTA GGCCTACTA

20

(2) INFORMATION FOR SEQ ID NO: 922:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:922:

ACAGGTGTAG GTCCTACTAA

20

(2) INFORMATION FOR SEQ ID NO: 923:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

105120.4248760

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:923:

CAGGTGTAGG TCCTACTAAT

20

(2) INFORMATION FOR SEQ ID NO: 924:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:924:

AGGTGTAGGT CCTACTAATA

20

(2) INFORMATION FOR SEQ ID NO: 925:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:925:

GGTGTAGGTC CTACTAATAC

20

(2) INFORMATION FOR SEQ ID NO: 926:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:926:

GTGTAGGTCC TACTAATACT

20

(2) INFORMATION FOR SEQ ID NO: 927:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:927:

TGTAGGTCCT ACTAATACTG

20

(2) INFORMATION FOR SEQ ID NO: 928:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:928:

GTAGGTCCTA CTAATACTGT

20

(2) INFORMATION FOR SEQ ID NO: 929:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:929:

TAGGTCCTAC TAATACTGTA

20

(2) INFORMATION FOR SEQ ID NO: 930:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:930:

AGGTCCTACT AATACTGTAC

20

(2) INFORMATION FOR SEQ ID NO: 931:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:931:

GGTCCTACTA ATACTGTACC

20

(2) INFORMATION FOR SEQ ID NO: 932:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:932:

GTCTACTAA TACTGTACCT

20

(2) INFORMATION FOR SEQ ID NO: 933:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:933:

TCCTACTAAT ACTGTACCTA

20

(2) INFORMATION FOR SEQ ID NO: 934:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:934:

CCTACTAATA CTGTACCTAT

20

(2) INFORMATION FOR SEQ ID NO: 935:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs

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(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:935:

CTACTAATAC TGTACCTATA

20

(2) INFORMATION FOR SEQ ID NO: 936:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:936:

TACTAATACT GTACCTATAG

20

(2) INFORMATION FOR SEQ ID NO: 937:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:937:

ACTAATACTG TACCTATAGC

20

(2) INFORMATION FOR SEQ ID NO: 938:

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AATACTGTAC CTATAGCTTT

20

(2) INFORMATION FOR SEQ ID NO: 941:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:941:

ATACTGTACC TATAGCTTTA

20

(2) INFORMATION FOR SEQ ID NO: 942:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:942:

TACTGTACCT ATAGCTTTAT

20

(2) INFORMATION FOR SEQ ID NO: 943:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:943:

ACTGTACCTA TAGCTTTATG

20

(2) INFORMATION FOR SEQ ID NO: 944:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:944:

CTGTACCTAT AGCTTTATGT

20

(2) INFORMATION FOR SEQ ID NO: 945:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:945:

TGTACCTATA GCTTTATGTC

20

(2) INFORMATION FOR SEQ ID NO: 946:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:946:

GTACCTATAG CTTTATGTCC

20

(2) INFORMATION FOR SEQ ID NO: 947:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:947:

TACCTATAGC TTTATGTCCA

20

(2) INFORMATION FOR SEQ ID NO: 948:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:948:

ACCTATAGCT TTATGTCCAC

20

(2) INFORMATION FOR SEQ ID NO: 949:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:949:

CCTATAGCTT TATGTCCACA

20

(2) INFORMATION FOR SEQ ID NO: 950:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:950:

CTATAGCTTT ATGTCCACAG

20

(2) INFORMATION FOR SEQ ID NO: 951:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:951:

TATAGCTTTA TGTCCACAGA

20

(2) INFORMATION FOR SEQ ID NO: 952:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:952:

ATAGCTTTAT GTCCACAGAT

20

(2) INFORMATION FOR SEQ ID NO: 953:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:953:

TAGCTTTATG TCCACAGATT

20

(2) INFORMATION FOR SEQ ID NO: 954:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:954:

AGCTTTATGT CCACAGATTT

20

(2) INFORMATION FOR SEQ ID NO: 955:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:955:

GCTTTATGTC CACAGATTTC

20

(2) INFORMATION FOR SEQ ID NO: 956:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:956:

CTTTATGTCC ACAGATTTC

20

(2) INFORMATION FOR SEQ ID NO: 957:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:957:

TTTATGTCCA CAGATTCTA

20

(2) INFORMATION FOR SEQ ID NO: 958:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:958:

TTATGTCCAC AGATTCTAT

20

(2) INFORMATION FOR SEQ ID NO: 959:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:959:

TATGTCCACA GATTCTATG

20

(2) INFORMATION FOR SEQ ID NO: 960:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:960:

ATGTCACAG ATTCTATGA

20

(2) INFORMATION FOR SEQ ID NO: 961:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:961:

TGTCACAGA TTTCTATGAG

20

(2) INFORMATION FOR SEQ ID NO: 962:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:962:

GTCCACAGAT TTCTATGAGT

20

(2) INFORMATION FOR SEQ ID NO: 963:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:963:

TCCACAGATT TCTATGASTA

20

(2) INFORMATION FOR SEQ ID NO: 964:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:964:

CCACAGATTT CTATAGTAT

20

(2) INFORMATION FOR SEQ ID NO: 965:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:965:

CACAGATTTC TATGAGTATC

20

(2) INFORMATION FOR SEQ ID NO: 966:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:966:

ACAGATTCTCT ATGAGTATCT

20

(2) INFORMATION FOR SEQ ID NO: 967:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:967:

CAGATTCTCTA TGAGTATCTG

20

(2) INFORMATION FOR SEQ ID NO: 968:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:968:

AGATTCTCTAT GAGTATCTGA

20

(2) INFORMATION FOR SEQ ID NO: 969:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:969:

GATTTCTATG AGTATCTGAT

20

(2) INFORMATION FOR SEQ ID NO: 970:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:970:

ATTTCTATGA GTATCTGATC

20

(2) INFORMATION FOR SEQ ID NO: 971:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:971:

TTTCTATGAG TATCTGATCA

20

(2) INFORMATION FOR SEQ ID NO: 972:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

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- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:972:

TTCTATGAGT ATCTGATCAT

20

(2) INFORMATION FOR SEQ ID NO: 973:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:973:

TCTATGAGTA TCTGATCATA

20

(2) INFORMATION FOR SEQ ID NO: 974:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:974:

CTATGAGTAT CTGATCATAC

20

(2) INFORMATION FOR SEQ ID NO: 975:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs

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(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:975:

TATGAGTATC TGATCATACT

20

(2) INFORMATION FOR SEQ ID NO: 976:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:976:

ATGAGTATCT GATCATACTG

20

(2) INFORMATION FOR SEQ ID NO: 977:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:977:

TGAGTATCTG ATCATACTGT

20

(2) INFORMATION FOR SEQ ID NO: 978:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:978:

GAGTATCTGA TCATACTGTC

20

(2) INFORMATION FOR SEQ ID NO: 979:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:979:

AGTATCTGAT CATACTGTCT

20

(2) INFORMATION FOR SEQ ID NO: 980:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:980:

GTATCTGATC ATACTGTCTT

20

(2) INFORMATION FOR SEQ ID NO: 981:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:981:

TATCTGATCA TACTGTCTTA

20

(2) INFORMATION FOR SEQ ID NO: 982:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:982:

ATCTGATCAT ACTGTCTTAC

20

(2) INFORMATION FOR SEQ ID NO: 983:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:983:

TCTGATCATA CTGTCTTACT

20

(2) INFORMATION FOR SEQ ID NO: 984:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:984:

CTGATCATAC TGTCTTACTT

20

(2) INFORMATION FOR SEQ ID NO: 985:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:985:

TGATCATACT GTCTTACTTT

20

(2) INFORMATION FOR SEQ ID NO: 986:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

03784874.021501

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:986:

GATCATACTG TCTTACTTTG

20

(2) INFORMATION FOR SEQ ID NO: 987:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:987:

ATCATACTGT CTTACTTTGA

20

(2) INFORMATION FOR SEQ ID NO: 988:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:988:

TCATACTGTC TTACTTTTGAT

20

(2) INFORMATION FOR SEQ ID NO: 989:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

09784674-021501

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:989:

CATACTGTCT TACTTTGATA

20

(2) INFORMATION FOR SEQ ID NO: 990:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:990:

ATACTGTCTT ACTTTGATAA

20

(2) INFORMATION FOR SEQ ID NO: 991:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:991:

TACTGTCTTA CTTTGATAAA

20

(2) INFORMATION FOR SEQ ID NO: 992:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

09784674.021501

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:992:

ACTGTCTTAC TTTGATAAAA

20

(2) INFORMATION FOR SEQ ID NO: 993:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:993:

CTGTCTTACT TTGATAAAAC

20

(2) INFORMATION FOR SEQ ID NO: 994:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:994:

TGCTCTTACTT TGATAAAACC

20

(2) INFORMATION FOR SEQ ID NO: 995:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:995:

GTCTTACTTT GATAAACCT

20

(2) INFORMATION FOR SEQ ID NO: 996:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:996:

TCTTACTTTG ATAAACCTC

20

(2) INFORMATION FOR SEQ ID NO: 997:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:997:

CTTACTTTGA TAAACCTCC

20

(2) INFORMATION FOR SEQ ID NO: 998:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:998:

TTACTTTGAT AAAACCTCCA

20

(2) INFORMATION FOR SEQ ID NO: 999:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:999:

TACTTTGATA AAACCTCCAA

20

(2) INFORMATION FOR SEQ ID NO: 1000:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1000:

ACTTTGATAA AACCTCCAAT

20

(2) INFORMATION FOR SEQ ID NO: 1001:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1001:

CTTTGATAAA ACCTCCAATT

20

(2) INFORMATION FOR SEQ ID NO: 1002:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1002:

TTTGATAAAA CCTCCAATTC

20

(2) INFORMATION FOR SEQ ID NO: 1003:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1003:

TTGATAAAAC CTCCAATTCC

20

(2) INFORMATION FOR SEQ ID NO: 1004:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1004:

TGATAAAACC TCCAATTCCC

20

(2) INFORMATION FOR SEQ ID NO: 1005:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1005:

GATAAAACCT CCAATTCCCC

20

(2) INFORMATION FOR SEQ ID NO: 1006:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1006:

ATAAAACCTC CAATCCCCC

20

(2) INFORMATION FOR SEQ ID NO: 1007:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1007:

TAAACCTCC AATCCCCCT

20

(2) INFORMATION FOR SEQ ID NO: 1008:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1008:

AAAACCTCCA ATTCCCCCTA

20

(2) INFORMATION FOR SEQ ID NO: 1009:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1009:

AAACCTCCAA TTCCCCCTAT

20

(2) INFORMATION FOR SEQ ID NO: 1010:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1010:

AACCTCCAAT TCCCCCTATC

20

(2) INFORMATION FOR SEQ ID NO: 1011:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1011:

ACCTCCAATT CCCCCTATCA

20

(2) INFORMATION FOR SEQ ID NO: 1012:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1012:

CCTCCAATTC CCCTATCAT

20

(2) INFORMATION FOR SEQ ID NO: 1013:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1013:

CTCCAATTCC CCCTATCATT

20

(2) INFORMATION FOR SEQ ID NO: 1014:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1014:

TCCAATTCCC CCTATCATTT

20

(2) INFORMATION FOR SEQ ID NO: 1015:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

10971464-1-021301

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1015:

CCAATTCCCC CTATCATTTT

20

(2) INFORMATION FOR SEQ ID NO: 1016:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1016:

CAATTCCCC TATCATTTTT

20

(2) INFORMATION FOR SEQ ID NO: 1017:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1017:

AATTCCCCCT ATCATTTTTT

20

(2) INFORMATION FOR SEQ ID NO: 1018:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1018:

ATTCCCCCTA TCATTTTGG

20

(2) INFORMATION FOR SEQ ID NO: 1019:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1019:

TTCCCCCTAT CATTITGGT

20

(2) INFORMATION FOR SEQ ID NO: 1020:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1020:

TCCCCCTATC ATTTTGGTT

20

(2) INFORMATION FOR SEQ ID NO: 1021:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1021:

CCCCCTATCA TTTTGGTTT

20

(2) INFORMATION FOR SEQ ID NO: 1022:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1022:

CCCCTATCAT TTTTGGTTTC

20

(2) INFORMATION FOR SEQ ID NO: 1023:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1023:

CCCTATCATT TTGGTTTCC

20

(2) INFORMATION FOR SEQ ID NO: 1024:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1024:

CCTATCATTT TTGGTTTCCA

20

(2) INFORMATION FOR SEQ ID NO: 1025:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1025:

CTATCATTTT TGTTTCCAT

20

(2) INFORMATION FOR SEQ ID NO: 1026:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1026:

TATCATTTTT GGTTCATC

20

(2) INFORMATION FOR SEQ ID NO: 1027:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1027:

ATCATTTTTG GTTCCATCT

20

(2) INFORMATION FOR SEQ ID NO: 1028:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1028:

TCATTTTTGG TTTCCATCTT

20

(2) INFORMATION FOR SEQ ID NO: 1029:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1029:

CATTTTGGT TTCCATCTTC

20

(2) INFORMATION FOR SEQ ID NO: 1030:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1030:

ATTTTGGTT TCCATCTTCC

20

(2) INFORMATION FOR SEQ ID NO: 1031:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1031:

TTTTTGGTTT CCATCTTCCT

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(2) INFORMATION FOR SEQ ID NO: 1032:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

00784674-021504

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1032:

TTTGTGTTTC CATCTTCCTG

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(2) INFORMATION FOR SEQ ID NO: 1033:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1033:

TTTGTGTTTC ATCTTCCTGG

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(2) INFORMATION FOR SEQ ID NO: 1034:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1034:

TTGTGTTTCCA TCTTCCTGGC

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(2) INFORMATION FOR SEQ ID NO: 1035:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs

10971464-1

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA  
(iii) HYPOTHETICAL: NO  
(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1035:

TGTTTCCAT CTCCTGGCA

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(2) INFORMATION FOR SEQ ID NO: 1036:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(iii) HYPOTHETICAL: NO  
(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1036:

GGTTTCCATC TTCCTGGCAA

20

(2) INFORMATION FOR SEQ ID NO: 1037:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(iii) HYPOTHETICAL: NO  
(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1037:

GTTTCCATCT TCCTGGCAAA

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(2) INFORMATION FOR SEQ ID NO: 1038:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1038:

TTTCCATCTT CCTGGCAAAC

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(2) INFORMATION FOR SEQ ID NO: 1039:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1039:

TTCCATCTTC CTGGCAAAC

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(2) INFORMATION FOR SEQ ID NO: 1040:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1040:

TCCATCTTCC TGGCAAATC

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(2) INFORMATION FOR SEQ ID NO: 1041:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1041:

CCATCTTCCT GGCAAATCA

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(2) INFORMATION FOR SEQ ID NO: 1042:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1042:

CATCTTCCTG GCAAATCAT

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(2) INFORMATION FOR SEQ ID NO: 1043:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1043:

ATCTTCCTGG CAAACTCATT

20

(2) INFORMATION FOR SEQ ID NO: 1044:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1044:

TCTTCCTGGC AAACCTCATT

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(2) INFORMATION FOR SEQ ID NO: 1045:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1045:

CTTCCTGGCA AACTCATTTC

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(2) INFORMATION FOR SEQ ID NO: 1046:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1046:

TTCTGGCAA ACTCATTCT

20

(2) INFORMATION FOR SEQ ID NO: 1047:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1047:

TCCTGGCAA CTCATTCTT

20

(2) INFORMATION FOR SEQ ID NO: 1048:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1048:

CCTGGCAAAC TCATTCTTC

20

(2) INFORMATION FOR SEQ ID NO: 1049:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1049:

CTGGCAAACCT CATTCTTCT

20

(2) INFORMATION FOR SEQ ID NO: 1050:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1050:

TGGCAAACCTC ATTTCTTCTA

20

(2) INFORMATION FOR SEQ ID NO: 1051:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1051:

GGCAAACCTCA TTTCTTCTAA

20

(2) INFORMATION FOR SEQ ID NO: 1052:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1052:

GCAAACTCAT TTCTTCTAAT

20

(2) INFORMATION FOR SEQ ID NO: 1053:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1053:

CAAACCTCATT TCTTCTAATA

20

(2) INFORMATION FOR SEQ ID NO: 1054:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1054:

AAACTCATTT CTCTAATAC

20

(2) INFORMATION FOR SEQ ID NO: 1055:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs

09784674.021501

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1055:

AACTCATTTC TTCTAATACT

20

(2) INFORMATION FOR SEQ ID NO: 1056:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1056:

ACTCATTCT TCTAATACTG

20

(2) INFORMATION FOR SEQ ID NO: 1057:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1057:

CTCATTCTT CTAATACTGT

20

(2) INFORMATION FOR SEQ ID NO: 1058:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1058:

TCATTCTTC TAATACTGTA

20

(2) INFORMATION FOR SEQ ID NO: 1059:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1059:

CATTCTCTCT AATACTGTAT

20

(2) INFORMATION FOR SEQ ID NO: 1060:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1060:

ATTTCTTCTA ATACTGTATC

20

(2) INFORMATION FOR SEQ ID NO: 1061:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1061:

TTTCTTCTAA TACTGTATCA

20

(2) INFORMATION FOR SEQ ID NO: 1062:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1062:

TTCTTCTAAT ACTGTATCAT

20

(2) INFORMATION FOR SEQ ID NO: 1063:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1063:

TCTTCTAATA CTGTATCATC

20

(2) INFORMATION FOR SEQ ID NO: 1064:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1064:

CTTCTAATAC TGTATCATCT

20

(2) INFORMATION FOR SEQ ID NO: 1065:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1065:

TTCTAATACT GTATCATCTG

20

(2) INFORMATION FOR SEQ ID NO: 1066:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1066:

TCTAATACTG TATCATCTGC

20

(2) INFORMATION FOR SEQ ID NO: 1067:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1067:

CTAATACTGT ATCATCTGCT

20

(2) INFORMATION FOR SEQ ID NO: 1068:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1068:

TAATACTGTA TCATCTGCTC

20

(2) INFORMATION FOR SEQ ID NO: 1069:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1069:

AATACTGTAT CATCTGCTCC

20

(2) INFORMATION FOR SEQ ID NO: 1070:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1070:

ATACTGTATC ATCTGCTCCT

20

(2) INFORMATION FOR SEQ ID NO: 1071:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1071:

TACTGTATCA TCTGCTCCTG

20

(2) INFORMATION FOR SEQ ID NO: 1072:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1072:

ACTGTATCAT CTGCTCCTGT

20

(2) INFORMATION FOR SEQ ID NO: 1073:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1073:

CTGTATCATC TGCTCCTGTA

20

(2) INFORMATION FOR SEQ ID NO: 1074:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1074:

TGTATCATCT GCTCCTGTAT

20

(2) INFORMATION FOR SEQ ID NO: 1075:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs

05784674.021501

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1075:

GTATCATCTG CTCCTGTATC

20

(2) INFORMATION FOR SEQ ID NO: 1076:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1076:

TATCATCTGC TCCTGTATCT

20

(2) INFORMATION FOR SEQ ID NO: 1077:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1077:

ATCATCTGCT CCTGTATCTA

20

(2) INFORMATION FOR SEQ ID NO: 1078:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1078:

TCATCTGCTC CTGTATCTAA

20

(2) INFORMATION FOR SEQ ID NO: 1079:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1079:

CATCTGCTCC TGTATCTAAT

20

(2) INFORMATION FOR SEQ ID NO: 1080:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1080:

09784674.021501

ATCTGCTCCT GTATCTAATA

20

(2) INFORMATION FOR SEQ ID NO: 1081:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1081:

TCTGCTCCTG TATCTAATAG

20

(2) INFORMATION FOR SEQ ID NO: 1082:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1082:

CTGCTCCTGT ATCTAATAGA

20

(2) INFORMATION FOR SEQ ID NO: 1083:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

10971464-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1083:

TGCTCCTGTA TCTAATAGAG

20

(2) INFORMATION FOR SEQ ID NO: 1084:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1084:

GCTCCTGTAT CTAATAGAGC

20

(2) INFORMATION FOR SEQ ID NO: 1085:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1085:

CTCCTGTATC TAATAGAGCT

20

(2) INFORMATION FOR SEQ ID NO: 1086:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1086:

TCCTGTATCT AATAGAGCTT

20

(2) INFORMATION FOR SEQ ID NO: 1087:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1087:

CCTGTATCTA ATAGAGCTTC

20

(2) INFORMATION FOR SEQ ID NO: 1088:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1088:

CTGTATCTAA TAGAGCTTCC

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(2) INFORMATION FOR SEQ ID NO: 1089:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1089:

TGTATCTAAT AGAGCTTCCT

20

(2) INFORMATION FOR SEQ ID NO: 1090:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1090:

GTATCTAATA GAGCTTCCTT

20

(2) INFORMATION FOR SEQ ID NO: 1091:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1091:

TATCTAATAG AGCTTCCTTT

20

(2) INFORMATION FOR SEQ ID NO: 1092:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1092:

ATCTAATAGA GCTTCCTTTA

20

(2) INFORMATION FOR SEQ ID NO: 1093:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1093:

TCTAATAGAG CTCCTTTAG

20

(2) INFORMATION FOR SEQ ID NO: 1094:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1094:

CTAATAGAGC TTCCTTTAGT

20

(2) INFORMATION FOR SEQ ID NO: 1095:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1095:

TAATAGAGCT TCCTTAGTT

20

(2) INFORMATION FOR SEQ ID NO: 1096:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1096:

AATAGAGCTT CCTTTAGTTG

20

(2) INFORMATION FOR SEQ ID NO: 1097:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1097:

ATAGAGCTTC CTTTAGTTGC

20

(2) INFORMATION FOR SEQ ID NO: 1098:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1098:

TAGAGCTTCC TTAGTTGCC

20

(2) INFORMATION FOR SEQ ID NO: 1099:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1099:

AGAGCTTCCT TTAGTTGCC

20

(2) INFORMATION FOR SEQ ID NO: 1100:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1100:

GAGCTTCCTT TAGTTGCCCC

20

(2) INFORMATION FOR SEQ ID NO: 1101:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1101:

AGCTTCCTTT AGTTGCCCCC

20

(2) INFORMATION FOR SEQ ID NO: 1102:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1102:

GCTTCCTTTA GTTGCCCCC

20

(2) INFORMATION FOR SEQ ID NO: 1103:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1103:

CTTCCTTTAG TTGCCCCCCT

20

(2) INFORMATION FOR SEQ ID NO: 1104:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1104:

TTCCTTTAGT TGCCCCCCTA

20

(2) INFORMATION FOR SEQ ID NO: 1105:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1105:

TCCTTTAGTT GCCCCCCCTAT

20

(2) INFORMATION FOR SEQ ID NO: 1106:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1106:

CCTTTAGTTG CCCCCTATC

20

(2) INFORMATION FOR SEQ ID NO: 1107:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1107:

CTTTAGTTGC CCCCCTATCT

20

(2) INFORMATION FOR SEQ ID NO: 1108:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1108:

TTTAGTTGCC CCCCTATCTT

20

(2) INFORMATION FOR SEQ ID NO: 1109:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

09734674.021501

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1109:

TTAGTTGCCC CCCTATCTTT

20

(2) INFORMATION FOR SEQ ID NO: 1110:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1110:

TAGTTGCCCC CCTATCTTTA

20

(2) INFORMATION FOR SEQ ID NO: 1111:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1111:

AGTTGCCCC CTATCTTTAT

20

(2) INFORMATION FOR SEQ ID NO: 1112:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1112:

GTGCCCCC TATCTTTATT

20

(2) INFORMATION FOR SEQ ID NO: 1113:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1113:

TTGCCCCCT ATCTTTATTG

20

(2) INFORMATION FOR SEQ ID NO: 1114:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1114:

TGCCCCCTA TCTTTATTGT

20

(2) INFORMATION FOR SEQ ID NO: 1115:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs

10971464-1

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1115:

GCCCCCTAT CTTATTGTG

20

(2) INFORMATION FOR SEQ ID NO: 1116:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1116:

CCCCCTATC TTTATTGTGA

20

(2) INFORMATION FOR SEQ ID NO: 1117:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1117:

CCCCCTATCT TTATTGTGAC

20

(2) INFORMATION FOR SEQ ID NO: 1118:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1118:

CCCCTATCTT TATTGTGACG

20

(2) INFORMATION FOR SEQ ID NO: 1119:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1119:

CCCTATCTTT ATTGTGACGA

20

(2) INFORMATION FOR SEQ ID NO: 1120:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1120:

CCTATCTTTA TTGTGACGAG

20

(2) INFORMATION FOR SEQ ID NO: 1121:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1121:

CTATCTTTAT TGTGACGAGG

20

(2) INFORMATION FOR SEQ ID NO: 1122:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1122:

TATCTTTATT GTGACGAGGG

20

(2) INFORMATION FOR SEQ ID NO: 1123:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1123:  
ATCTTTATTG TGACGAGGGG 20

(2) INFORMATION FOR SEQ ID NO: 1124:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1124:  
TCCTTTATTGT GACGAGGGGT 20

(2) INFORMATION FOR SEQ ID NO: 1125:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1125:  
CTTTATTGTG ACGAGGGGTC 20

(2) INFORMATION FOR SEQ ID NO: 1126:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1126:

TTTATTGTGA CGAGGGGTCG

20

(2) INFORMATION FOR SEQ ID NO: 1127:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1127:

TTATTGTGAC GAGGGGTCGT

20

(2) INFORMATION FOR SEQ ID NO: 1128:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1128:

TATTGTGACG AGGGGTCGTT

20

(2) INFORMATION FOR SEQ ID NO: 1129:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1129:

ATTGTGACGA GGGTCGTTG

20

(2) INFORMATION FOR SEQ ID NO: 1130:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1130:

TTGTGACGAG GGGTCGTTGC

20

(2) INFORMATION FOR SEQ ID NO: 1131:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1131:

TGTGACGAGG GGTCTTGCC

20

(2) INFORMATION FOR SEQ ID NO: 1132:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

09784674-021504

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1132:

GTGACGAGGG GTCGTTGCCA

20

(2) INFORMATION FOR SEQ ID NO: 1133:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1133:

TGACGAGGGG TCGTTGCCAA

20

(2) INFORMATION FOR SEQ ID NO: 1134:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1134:

GACGAGGGGT CGTTGCCAAA

20

(2) INFORMATION FOR SEQ ID NO: 1135:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs

105120.4/2448260

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1135:

ACGAGGGGTC GTTGCCAAAG

20

(2) INFORMATION FOR SEQ ID NO: 1136:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1136:

CGAGGGGTCG TIGCCAAAGA

20

(2) INFORMATION FOR SEQ ID NO: 1137:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1137:

GAGGGGTCGT TGCCAAAGAG

20

(2) INFORMATION FOR SEQ ID NO: 1138:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1138:

AGGGGTCGTT GCCAAGAGT

20

(2) INFORMATION FOR SEQ ID NO: 1139:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1139:

GGGGTCGTTG CCAAGAGTG

20

(2) INFORMATION FOR SEQ ID NO: 1140:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1140:

GGGTCGTTGC CAAAGAGTGA

20

(2) INFORMATION FOR SEQ ID NO: 1141:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1141:

GGTCGTTGCC AAAGAGTGAT

20

(2) INFORMATION FOR SEQ ID NO: 1142:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1142:

GTCGTTGCCA AAGAGTGATC

20

(2) INFORMATION FOR SEQ ID NO: 1143:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

10971464-021501

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1143:

TCGTTGCCAA AGAGTGATCT

20

(2) INFORMATION FOR SEQ ID NO: 1144:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1144:

CGTTGCCAAA GAGTGATCTG

20

(2) INFORMATION FOR SEQ ID NO: 1145:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1145:

GTTGCCAAAG AGTGATCTGA

20

(2) INFORMATION FOR SEQ ID NO: 1146:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1146:

TTGCCAAAGA GTGATCTGAG

20

(2) INFORMATION FOR SEQ ID NO: 1147:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1147:

TGCCAAAGAG TGATCTGAGG

20

(2) INFORMATION FOR SEQ ID NO: 1148:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1148:

GCCAAAGAGT GATCTGAGGG

20

(2) INFORMATION FOR SEQ ID NO: 1149:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1149:

CCAAAGAGTG ATCTGAGGGA

20

(2) INFORMATION FOR SEQ ID NO: 1150:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1150:

CAAAGAGTGA TCTGAGGGAA

20

(2) INFORMATION FOR SEQ ID NO: 1151:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1151:

AAAGAGTGAT CTGAGGGAAG

20

(2) INFORMATION FOR SEQ ID NO: 1152:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

105120.4798763

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1152:

AAGAGTGATC TGAGGGAAGT

20

(2) INFORMATION FOR SEQ ID NO: 1153:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1153:

AGAGTGATCT GAGGGAAGTT

20

(2) INFORMATION FOR SEQ ID NO: 1154:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1154:

GAGTGATCTG AGGGAAGTTA

20

(2) INFORMATION FOR SEQ ID NO: 1155:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs

10971464-1

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1155:

AGTGATCTGA GGAAGTTAA

20

(2) INFORMATION FOR SEQ ID NO: 1156:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1156:

GTGATCTGAG GGAAGTTAAA

20

(2) INFORMATION FOR SEQ ID NO: 1157:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1157:

TGATCTGAGG GAAGTTAAG

20

(2) INFORMATION FOR SEQ ID NO: 1158:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1158:

GATCTGAGGG AAGTTAAAGG

20

(2) INFORMATION FOR SEQ ID NO: 1159:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1159:

ATCTGAGGGA AGTTAAGGA

20

(2) INFORMATION FOR SEQ ID NO: 1160:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1160:

10971464-021501

TCTGAGGGAA GTTAAAGGAT

20

(2) INFORMATION FOR SEQ ID NO: 1161:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1161:

CTGAGGGAAG TTAAGGATA

20

(2) INFORMATION FOR SEQ ID NO: 1162:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1162:

TGAGGGAAGT TAAAGGATAC

20

(2) INFORMATION FOR SEQ ID NO: 1163:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:1163:

GAGGGAAGTT AAAGGATACA

20

(2) INFORMATION FOR SEQ ID NO: 1164:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:1164:

AGGGAAGTTA AAGGATACAG

20

(2) INFORMATION FOR SEQ ID NO: 1165:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:1165:

GGGAAGTTAA AGGATACAGT

20